

SEQUENCE LISTING

<110> Allan, Bernard
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Wong, Chi-Wai
Metabolex, Inc.

<120> Methods of Diagnosing and Treating Diabetes and Insulin
Resistance

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<141> 2005-01-26

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<151> 2002-06-04

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<210> 14

<211> 520

<212> PRT

<213> Homo sapiens

<220>

<223> human succinyl CoA:3-oxoacid CoA transferase
(OXCT)

<400> 14

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20 25 30

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 Ala Val Lys Asp Ile Pro Asp Gly Ala Thr Val Leu Val Gly Gly Phe
 50 55 60
 Gly Leu Cys Gly Ile Pro Glu Asn Leu Ile Asp Ala Leu Leu Lys Thr
 65 70 75 80
 Gly Val Lys Gly Leu Thr Ala Val Ser Asn Asn Ala Gly Val Asp Asn
 85 90 95
 Phe Gly Leu Gly Leu Leu Leu Arg Ser Lys Gln Ile Lys Arg Met Val
 100 105 110
 Ser Ser Tyr Val Gly Glu Asn Ala Glu Phe Glu Arg Gln Tyr Leu Ser
 115 120 125
 Gly Glu Leu Glu Val Glu Leu Thr Pro Gln Gly Thr Leu Ala Glu Arg
 130 135 140
 Ile Arg Ala Gly Gly Ala Gly Val Pro Ala Phe Tyr Thr Pro Thr Gly
 145 150 155 160
 Tyr Gly Thr Leu Val Gln Glu Gly Gly Ser Pro Ile Lys Tyr Asn Lys
 165 170 175
 Asp Gly Ser Val Ala Ile Ala Ser Lys Pro Arg Glu Val Arg Glu Phe
 180 185 190
 Asn Gly Gln His Phe Ile Leu Glu Glu Ala Ile Thr Gly Asp Phe Ala
 195 200 205
 Leu Val Lys Ala Trp Lys Ala Asp Arg Ala Gly Asn Val Ile Phe Arg
 210 215 220
 Lys Ser Ala Arg Asn Phe Asn Leu Pro Met Cys Lys Ala Ala Glu Thr
 225 230 235 240
 Thr Val Val Glu Val Glu Glu Ile Val Asp Ile Gly Ala Phe Ala Pro
 245 250 255
 Glu Asp Ile His Ile Pro Gln Ile Tyr Val His Arg Leu Ile Lys Gly
 260 265 270
 Glu Lys Tyr Glu Lys Arg Ile Glu Arg Leu Ser Ile Arg Lys Glu Gly
 275 280 285
 Asp Gly Glu Ala Lys Ser Ala Lys Pro Gly Asp Asp Val Arg Glu Arg
 290 295 300
 Ile Ile Lys Arg Ala Ala Leu Glu Phe Glu Asp Gly Met Tyr Ala Asn
 305 310 315 320
 Leu Gly Ile Gly Ile Pro Leu Leu Ala Ser Asn Phe Ile Ser Pro Asn
 325 330 335
 Ile Thr Val His Leu Gln Ser Glu Asn Gly Val Leu Gly Leu Gly Pro
 340 345 350

Tyr Pro Arg Gln His Glu Ala Asp Ala Asp Leu Ile Asn Ala Gly Lys
 355 360 365
 Glu Thr Val Thr Ile Leu Pro Gly Ala Ser Phe Phe Ser Ser Asp Glu
 370 375 380
 Ser Phe Ala Met Ile Arg Gly Gly His Val Asp Leu Thr Met Leu Gly
 385 390 395 400
 Ala Met Gln Val Ser Lys Tyr Gly Asp Leu Ala Asn Trp Met Ile Pro
 405 410 415
 Gly Lys Met Val Lys Gly Met Gly Gly Ala Met Asp Leu Val Ser Ser
 420 425 430
 Ala Lys Thr Lys Val Val Val Thr Met Glu His Ser Ala Lys Gly Asn
 435 440 445
 Ala His Lys Ile Met Glu Lys Cys Thr Leu Pro Leu Thr Gly Lys Gln
 450 455 460
 Cys Val Asn Arg Ile Ile Thr Glu Lys Ala Val Phe Asp Val Asp Lys
 465 470 475 480
 Lys Lys Gly Leu Thr Leu Ile Glu Leu Trp Glu Gly Leu Thr Val Asp
 485 490 495
 Asp Val Gln Lys Ser Thr Gly Cys Asp Phe Ala Val Ser Pro Lys Leu
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 Met Pro Met Gln Gln Ile Ala Asn
 515 520

<210> 15
 <211> 1823
 <212> DNA
 <213> Mus musculus

<220>
 <223> mouse succinyl CoA:3-oxoacid CoA transferase
 (OXCT, SCOT) cDNA

<220>
 <221> CDS
 <222> (49)..(1611)
 <223> OXCT

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 aagccacgag aggtgagggg gtttaacggt cagcacttca ttttggagga agccatcacg 660
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cgaaaggaag gagatggaaa aggcaaatcc ggtaagcctg gaggcgatgt gaggggaacgg 960
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atgtcagtaa tcaatagtta cattacacat ttagcaagaa gtttcggcta gttttcttct 1740
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<210> 16

<211> 520

<212> PRT

<213> Mus musculus

<220>

<223> mouse succinyl CoA:3-oxoacid CoA transferase
(OXCT, SCOT)

<400> 16

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Met Ala Ala Leu Lys Leu Leu Ser Ser Gly Leu Arg Leu Gly Ala Ser
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Ala Arg Ser Ser Arg Gly Ala Leu His Lys Gly Cys Val Cys Tyr Phe
          20                      25                      30

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Ser Val Ser Thr Arg His His Thr Lys Phe Tyr Thr Asp Pro Val Glu
          35                      40                      45

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```

Ala Val Lys Asp Ile Pro Asn Gly Ala Thr Leu Leu Val Gly Gly Phe
          50                      55                      60

```

```

Gly Leu Cys Gly Ile Pro Glu Asn Leu Ile Gly Ala Leu Leu Lys Thr
          65                      70                      75                      80

```

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Gly Val Lys Asp Leu Thr Ala Val Ser Asn Asn Ala Gly Val Asp Asn
          85                      90                      95

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Phe Gly Leu Gly Leu Leu Leu Arg Ser Lys Gln Ile Lys Arg Met Ile
          100                      105                      110

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Ser Ser Tyr Val Gly Glu Asn Ala Glu Phe Glu Arg Gln Phe Leu Ser
          115                      120                      125

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Gly Glu Leu Glu Val Glu Leu Thr Pro Gln Gly Thr Leu Ala Glu Arg
          130                      135                      140

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Ile Arg Ala Gly Gly Ala Gly Val Pro Ala Phe Tyr Thr Ser Thr Gly
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Tyr Gly Thr Leu Val Gln Glu Gly Gly Ser Pro Ile Lys Tyr Asn Lys
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 Asp Gly Ser Val Ala Ile Ala Ser Lys Pro Arg Glu Val Arg Glu Phe
 180 185 190
 Asn Gly Gln His Phe Ile Leu Glu Glu Ala Ile Thr Gly Asp Phe Ala
 195 200 205
 Leu Val Lys Ala Trp Lys Ala Asp Arg Ala Gly Asn Val Ile Phe Arg
 210 215 220
 Lys Ser Ala Arg Asn Phe Asn Leu Pro Met Cys Lys Ala Ala Gly Thr
 225 230 235 240
 Thr Val Val Glu Val Glu Glu Ile Val Asp Ile Gly Ser Phe Ala Pro
 245 250 255
 Glu Asp Ile His Ile Pro Lys Ile Tyr Val His Arg Leu Ile Lys Gly
 260 265 270
 Glu Lys Tyr Glu Lys Arg Ile Glu Arg Leu Ser Leu Arg Lys Glu Gly
 275 280 285
 Asp Gly Lys Gly Lys Ser Gly Lys Pro Gly Gly Asp Val Arg Glu Arg
 290 295 300
 Ile Ile Lys Arg Ala Ala Leu Glu Phe Glu Asp Gly Met Tyr Ala Asn
 305 310 315 320
 Leu Gly Ile Gly Ile Pro Leu Leu Ala Ser Asn Phe Ile Ser Pro Asn
 325 330 335
 Met Thr Val His Leu Gln Ser Glu Asn Gly Val Leu Gly Leu Gly Pro
 340 345 350
 Tyr Pro Leu Lys Asp Glu Ala Asp Ala Asp Leu Ile Asn Ala Gly Lys
 355 360 365
 Glu Thr Val Thr Val Leu Pro Gly Ala Ser Phe Phe Ser Ser Asp Glu
 370 375 380
 Ser Phe Ala Met Ile Arg Gly Gly His Val Asn Leu Thr Met Leu Gly
 385 390 395 400
 Ala Met Gln Val Ser Lys Tyr Gly Asp Leu Ala Asn Trp Met Ile Pro
 405 410 415
 Gly Lys Met Val Lys Gly Met Gly Gly Ala Met Asp Leu Val Ser Ser
 420 425 430
 Ser Lys Thr Lys Val Val Val Thr Met Glu His Ser Ala Lys Gly Asn
 435 440 445
 Ala His Lys Ile Met Glu Lys Cys Thr Leu Pro Leu Thr Gly Lys Gln
 450 455 460
 Cys Val Asn Arg Ile Ile Thr Glu Lys Gly Val Phe Asp Val Asp Lys
 465 470 475 480

Lys Asn Gly Leu Thr Leu Ile Glu Leu Trp Glu Gly Leu Thr Val Asp
 485 490 495
 Asp Ile Lys Lys Ser Thr Gly Cys Asp Phe Ala Val Ser Pro Asn Leu
 500 505 510
 Met Pro Met Gln Gln Ile Ser Thr
 515 520

<210> 17
 <211> 2328
 <212> DNA
 <213> Homo sapiens

<220>
 <223> human acid ceramidase cDNA

<220>
 <221> CDS
 <222> (36)..(1223)
 <223> ceramidase

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 aggactgcag aaaatcaacc tatcctcctt caggaccaac gtacagaggt gcagttccat 180
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 aagtaaaaca gtcattctaga attcactgag ttttggttca ctttgacatt tggggatctg 1500
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 agcattcatg taataaacag gtttttagtt tgttcttcag attgataggg agtttttaag 2100
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catttggtgca agaccgtttg tccacttcat tttgtataat cacagttgtg ttcctgacac 2280
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<211> 395
<212> PRT
<213> Homo sapiens

<220>
<223> human acid ceramidase

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Lys Ser Thr Tyr Pro Pro Ser Gly Pro Thr Tyr Arg Gly Ala Val Pro
35 40 45
Trp Tyr Thr Ile Asn Leu Asp Leu Pro Pro Tyr Lys Arg Trp His Glu
50 55 60
Leu Met Leu Asp Lys Ala Pro Met Leu Lys Val Ile Val Asn Ser Leu
65 70 75 80
Lys Asn Met Ile Asn Thr Phe Val Pro Ser Gly Lys Val Met Gln Val
85 90 95
Val Asp Glu Lys Leu Pro Gly Leu Leu Gly Asn Phe Pro Gly Pro Phe
100 105 110
Glu Glu Glu Met Lys Gly Ile Ala Ala Val Thr Asp Ile Pro Leu Gly
115 120 125
Glu Ile Ile Ser Phe Asn Ile Phe Tyr Glu Leu Phe Thr Ile Cys Thr
130 135 140
Ser Ile Val Ala Glu Asp Lys Lys Gly His Leu Ile His Gly Arg Asn
145 150 155 160
Met Asp Phe Gly Val Phe Leu Gly Trp Asn Ile Asn Asn Asp Thr Trp
165 170 175
Val Ile Thr Glu Gln Leu Lys Pro Leu Thr Val Asn Leu Asp Phe Gln
180 185 190
Arg Asn Asn Lys Thr Val Phe Lys Ala Ser Ser Phe Ala Gly Tyr Val
195 200 205
Gly Met Leu Thr Gly Phe Lys Pro Gly Leu Phe Ser Leu Thr Leu Asn
210 215 220
Glu Arg Phe Ser Ile Asn Gly Gly Tyr Leu Gly Ile Leu Glu Trp Ile
225 230 235 240
Leu Gly Lys Lys Asp Ala Met Trp Ile Gly Phe Leu Thr Arg Thr Val
245 250 255

Leu Glu Asn Ser Thr Ser Tyr Glu Glu Ala Lys Asn Leu Leu Thr Lys
 260 265 270
 Thr Lys Ile Leu Ala Pro Ala Tyr Phe Ile Leu Gly Gly Asn Gln Ser
 275 280 285
 Gly Glu Gly Cys Val Ile Thr Arg Asp Arg Lys Glu Ser Leu Asp Val
 290 295 300
 Tyr Glu Leu Asp Ala Lys Gln Gly Arg Trp Tyr Val Val Gln Thr Asn
 305 310 315 320
 Tyr Asp Arg Trp Lys His Pro Phe Phe Leu Asp Asp Arg Arg Thr Pro
 325 330 335
 Ala Lys Met Cys Leu Asn Arg Thr Ser Gln Glu Asn Ile Ser Phe Glu
 340 345 350
 Thr Met Tyr Asp Val Leu Ser Thr Lys Pro Val Leu Asn Lys Leu Thr
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 Val Tyr Thr Thr Leu Ile Asp Val Thr Lys Gly Gln Phe Glu Thr Tyr
 370 375 380
 Leu Arg Asp Cys Pro Asp Pro Cys Ile Gly Trp
 385 390 395

<210> 19
 <211> 2176
 <212> DNA
 <213> Mus musculus

<220>
 <223> mouse N-acylsphingosine amidohydrolase (ASAH),
 acid ceramidase cDNA

<220>
 <221> CDS
 <222> (44)..(1228)
 <223> ceramidase

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<210> 20
 <211> 394
 <212> PRT
 <213> Mus musculus

<220>
 <223> mouse N-acylsphingosine amidohydrolase (ASAH),
 acid ceramidase

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 20 25 30
 Ser Thr Tyr Pro Pro Ser Gly Pro Thr Tyr Arg Gly Pro Val Pro Trp
 35 40 45
 His Thr Ile Asn Leu Asp Leu Pro Pro Tyr Lys Arg Trp His Glu Leu
 50 55 60
 Leu Ala Gln Lys Ala Pro Ala Leu Arg Ile Leu Val Asn Ser Ile Thr
 65 70 75 80
 Ser Leu Val Asn Thr Phe Val Pro Ser Gly Lys Leu Met Lys Met Val
 85 90 95
 Asp Gln Lys Leu Pro Gly Met Ile Gly Ser Leu Pro Asp Pro Phe Gly
 100 105 110
 Glu Glu Met Arg Gly Ile Ala Asp Val Thr Gly Ile Pro Leu Gly Glu
 115 120 125
 Ile Ile Ser Phe Asn Ile Phe Tyr Glu Leu Phe Thr Met Cys Thr Ser
 130 135 140
 Ile Ile Thr Glu Asp Glu Lys Gly His Leu Leu His Gly Arg Asn Met
 145 150 155 160

Asp Phe Gly Ile Phe Leu Gly Trp Asn Ile Asn Asn Asn Thr Trp Val
 165 170 175
 Val Thr Glu Glu Leu Lys Pro Leu Thr Val Asn Leu Asp Phe Gln Arg
 180 185 190
 Asn Asn Lys Thr Val Phe Lys Ala Thr Ser Phe Val Gly Tyr Val Gly
 195 200 205
 Met Leu Thr Gly Phe Lys Pro Gly Leu Phe Ser Leu Ser Leu Asn Glu
 210 215 220
 Arg Phe Ser Ile Asn Gly Gly Tyr Leu Gly Ile Leu Glu Trp Met Phe
 225 230 235 240
 Gly Arg Lys Asp Ala Gln Trp Val Gly Phe Ile Thr Arg Ser Val Leu
 245 250 255
 Glu Asn Thr Thr Ser Tyr Glu Glu Ala Lys Asn Thr Leu Thr Lys Thr
 260 265 270
 Lys Ile Met Ala Pro Val Tyr Phe Ile Leu Gly Gly Lys Lys Ser Gly
 275 280 285
 Glu Gly Cys Val Ile Thr Arg Glu Arg Lys Glu Ser Leu Asp Val Tyr
 290 295 300
 Glu Leu Asp Pro Lys His Gly Arg Trp Tyr Val Val Gln Thr Asn Tyr
 305 310 315 320
 Asp Arg Trp Lys Asn Thr Leu Phe Ile Asp Asp Arg Arg Thr Pro Ala
 325 330 335
 Lys Lys Cys Leu Asn His Thr Thr Gln Lys Asn Leu Ser Phe Ala Thr
 340 345 350
 Ile Tyr Asp Val Leu Ser Thr Lys Pro Val Leu Asn Lys Leu Thr Val
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 370 375 380
 Arg Asp Cys Pro Asp Pro Cys Ile Gly Trp
 385 390

<210> 21
 <211> 1280
 <212> DNA
 <213> Rattus norvegicus

<220>
 <223> rat N-acylsphingosine amidohydrolase (ASAH), acid
 ceramidase cDNA

<220>
 <221> CDS
 <222> (15)..(1199)
 <223> ceramidase

<400> 21
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 ctcttcttgg accaacctat agaggaccag ttccgtggta caccataaat cttgatttac 180
 caccctacaa gagatggcat gaattattgg ctcacaaggc acctgtgttg agaactttag 240
 tgaattccat ctgcaattta gtgaatgcat ttgtgccaag tggaaaaata atgcagatgg 300
 tggatgaaaa gttgcctggg ctgattggca gcattcctgg cccttttggg gaggaaatga 360
 gggggattgc agatgttact gggattcctc taggagagat tatttcattc aacattttct 420
 atgaactggt caccatgtgt acatcgatca taactgaaga tggaaaagggt catttactac 480
 atggaagaaa catggatttt ggaatatttc ttgggtggaa cattaacaac aacacttggg 540
 tgggtgacaga agaattaaag cttttaacag tgaatttggg cttccagagg aacaataaga 600
 ctgtgttcaa ggctacaagt ttcgctggat acgtgggcat gttgacagga ttcaaaccag 660
 gactgttaag tcttacctg aatgaacggt tcagttttaa tgggtggttat ctgggtatcc 720
 tagaattggt gtttggaaaag aaaaatgccc aatgggtagg gtttatcact agatcagttc 780
 tggaaaatag cacaagttat gaagaagcca agaatatatt gaccaagacc aagataacgg 840
 ccccagcata ttttatcctg ggaggcaacc agtctggaga aggttgtgtg attacacgag 900
 aaagaaaaga gtcttttagac gtctatgaac ttgatcctaa gcatggcaga tggtagctgg 960
 tacaaccaa ttatgaccgg tggaaaaaca ccttggttct tgatgaccgc agaacacctg 1020
 cgaagaagtg tctaaatcac acgacacaga agaatctgtc atttgctacc atctatgatg 1080
 ttctatcaac aaaacctgtc ctcaacaagc tgactgtatt cacaaccttg atagatggga 1140
 ccaaagatcc atttgaaagc caccttcgag attgcccaga cccttgtata ggctgggtgag 1200
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 gcgtgggtctc cttccatagg 1280

<210> 22
 <211> 394
 <212> PRT
 <213> Rattus norvegicus

<220>
 <223> rat N-acylsphingosine amidohydrolase (ASAH), acid
 ceramidase

<400> 22
 Met Leu Gly Arg Ser Leu Leu Thr Trp Val Leu Ala Ala Ala Val Thr
 1 5 10 15
 Cys Ala Gln Ala Gln Gln Val Pro Pro Trp Thr Glu Asp Cys Arg Lys
 20 25 30
 Ser Thr Tyr Pro Pro Ser Gly Pro Thr Tyr Arg Gly Pro Val Pro Trp
 35 40 45
 Tyr Thr Ile Asn Leu Asp Leu Pro Pro Tyr Lys Arg Trp His Glu Leu
 50 55 60
 Leu Ala His Lys Ala Pro Val Leu Arg Thr Leu Val Asn Ser Ile Ser
 65 70 75 80
 Asn Leu Val Asn Ala Phe Val Pro Ser Gly Lys Ile Met Gln Met Val
 85 90 95
 Asp Glu Lys Leu Pro Gly Leu Ile Gly Ser Ile Pro Gly Pro Phe Gly
 100 105 110
 Glu Glu Met Arg Gly Ile Ala Asp Val Thr Gly Ile Pro Leu Gly Glu
 115 120 125
 Ile Ile Ser Phe Asn Ile Phe Tyr Glu Leu Phe Thr Met Cys Thr Ser
 130 135 140

Ile	Ile	Thr	Glu	Asp	Gly	Lys	Gly	His	Leu	Leu	His	Gly	Arg	Asn	Met	145	150	155	160
Asp	Phe	Gly	Ile	Phe	Leu	Gly	Trp	Asn	Ile	Asn	Asn	Asn	Thr	Trp	Val	165	170		175
Val	Thr	Glu	Glu	Leu	Lys	Pro	Leu	Thr	Val	Asn	Leu	Asp	Phe	Gln	Arg	180	185		190
Asn	Asn	Lys	Thr	Val	Phe	Lys	Ala	Thr	Ser	Phe	Ala	Gly	Tyr	Val	Gly	195	200		205
Met	Leu	Thr	Gly	Phe	Lys	Pro	Gly	Leu	Leu	Ser	Leu	Thr	Leu	Asn	Glu	210	215		220
Arg	Phe	Ser	Leu	Asn	Gly	Gly	Tyr	Leu	Gly	Ile	Leu	Glu	Trp	Met	Phe	225	230		235
Gly	Lys	Lys	Asn	Ala	Gln	Trp	Val	Gly	Phe	Ile	Thr	Arg	Ser	Val	Leu	245	250		255
Glu	Asn	Ser	Thr	Ser	Tyr	Glu	Glu	Ala	Lys	Asn	Ile	Leu	Thr	Lys	Thr	260	265		270
Lys	Ile	Thr	Ala	Pro	Ala	Tyr	Phe	Ile	Leu	Gly	Gly	Asn	Gln	Ser	Gly	275	280		285
Glu	Gly	Cys	Val	Ile	Thr	Arg	Glu	Arg	Lys	Glu	Ser	Leu	Asp	Val	Tyr	290	295		300
Glu	Leu	Asp	Pro	Lys	His	Gly	Arg	Trp	Tyr	Val	Val	Gln	Thr	Asn	Tyr	305	310		315
Asp	Arg	Trp	Lys	Asn	Thr	Leu	Phe	Leu	Asp	Asp	Arg	Arg	Thr	Pro	Ala	325	330		335
Lys	Lys	Cys	Leu	Asn	His	Thr	Thr	Gln	Lys	Asn	Leu	Ser	Phe	Ala	Thr	340	345		350
Ile	Tyr	Asp	Val	Leu	Ser	Thr	Lys	Pro	Val	Leu	Asn	Lys	Leu	Thr	Val	355	360		365
Phe	Thr	Thr	Leu	Ile	Asp	Gly	Thr	Lys	Asp	Pro	Phe	Glu	Ser	His	Leu	370	375		380
Arg	Asp	Cys	Pro	Asp	Pro	Cys	Ile	Gly	Trp							385	390		

<210> 23

<211> 1418

<212> DNA

<213> Homo sapiens

<220>

<223> human map kinase phosphatase-like protein MK-STYX
cDNA

<220>
 <221> CDS
 <222> (340)..(1281)
 <223> MK-STYX

 <220>
 <221> modified_base
 <222> (1)..(1418)
 <223> n = g, a, c or t

<400> 23
 gccacttccg ggagtcggaa aggaaagctg tgggaccatc ctggcaaccc cgggtgtttgg 60
 ctgggttcta gcgtaccggg ctgtgtggcc ggtggggggac ctgcggtcgg agtgggaggg 120
 ccagtctgca cccaagaggt ggaagaggac gggcttttagg ctggaacgcc ttagaggagc 180
 cattttttcca ggtggggccc cagnagaggc tccgacagga gctgngccat agtcgcgcga 240
 cggggaggtg gagcgcgtcc cagacccgan ccccccaccc cagccaaacc cattccttct 300
 gtccttggag gccagagggg actctgagca tcggaaagga tgcctggttt gcttttatgt 360
 gaaccgacag agcttttaca catcctgaat caggccacaa aactctccag attaacagac 420
 cccaactatc tctgtttatt ggatgtccgt tccaaatggg agtatgacga aagccatgtg 480
 atcactgccc ttcgagtga gaagaaaaat aatgaatatc ttctcccgga gtctgtggac 540
 ctggagtgtg tgaagtactg cgtggtgtat gataacaaca gcagcaccct ggagatactc 600
 ttaaaagatg atgatgatga ttcagactct gatggtgatg gcaaagatct tgtgcctcaa 660
 gcagccattg agtatggcag gatcctgacc cgctcacc accaccccggt ctacatcctg 720
 aaagggggct atgagcgctt ctcaggcacg taccactttc tccggaccca gaagatcatc 780
 tggatgcctc aggaactgga tgcatttcag ccatacccca ttgaaatcgt gccagggag 840
 gtcttcgttg gcaatttcag tcaagcctgt gaccccaaga ttcagaagga cttgaaaatc 900
 aaagcccatg tcaatgtctc catggataga gggccctttt ttgcaggcga tgctgacaag 960
 cttctgcaca tccggataga agattccccg gaagcccaga ttcttccctt cttacgccac 1020
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 cagggtatca gccgcagttg tgccgccatc atagcctacc tcatgcatag taacgagcag 1140
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 ggattggtga gccagctgct ggaatgggag aagactatcc ttggagattc catcacaac 1260
 atcatggatc cgctctactg atcttctccg aggccaccg aagggtactg aagagcctca 1320
 cctgggggca ttttgtgggt ggagggccag agtgtgtata cccaggcttg tctggaagga 1380
 gaaggccttt gctgcctgaa agtctcaaaa aaaaaaaaa 1418

<210> 24
 <211> 313
 <212> PRT
 <213> Homo sapiens

<220>
 <223> human map kinase phosphatase-like protein MK-STYX

<400> 24
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 1 5 10 15
 Asn Gln Ala Thr Lys Leu Ser Arg Leu Thr Asp Pro Asn Tyr Leu Cys
 20 25 30
 Leu Leu Asp Val Arg Ser Lys Trp Glu Tyr Asp Glu Ser His Val Ile
 35 40 45
 Thr Ala Leu Arg Val Lys Lys Lys Asn Asn Glu Tyr Leu Leu Pro Glu
 50 55 60
 Ser Val Asp Leu Glu Cys Val Lys Tyr Cys Val Val Tyr Asp Asn Asn
 65 70 75 80

Ser Ser Thr Leu Glu Ile Leu Leu Lys Asp Asp Asp Asp Asp Ser Asp
 85 90 95
 Ser Asp Gly Asp Gly Lys Asp Leu Val Pro Gln Ala Ala Ile Glu Tyr
 100 105 110
 Gly Arg Ile Leu Thr Arg Leu Thr His His Pro Val Tyr Ile Leu Lys
 115 120 125
 Gly Gly Tyr Glu Arg Phe Ser Gly Thr Tyr His Phe Leu Arg Thr Gln
 130 135 140
 Lys Ile Ile Trp Met Pro Gln Glu Leu Asp Ala Phe Gln Pro Tyr Pro
 145 150 155 160
 Ile Glu Ile Val Pro Gly Lys Val Phe Val Gly Asn Phe Ser Gln Ala
 165 170 175
 Cys Asp Pro Lys Ile Gln Lys Asp Leu Lys Ile Lys Ala His Val Asn
 180 185 190
 Val Ser Met Asp Thr Gly Pro Phe Phe Ala Gly Asp Ala Asp Lys Leu
 195 200 205
 Leu His Ile Arg Ile Glu Asp Ser Pro Glu Ala Gln Ile Leu Pro Phe
 210 215 220
 Leu Arg His Met Cys His Phe Ile Glu Ile His His His Leu Gly Ser
 225 230 235 240
 Val Ile Leu Ile Phe Ser Thr Gln Gly Ile Ser Arg Ser Cys Ala Ala
 245 250 255
 Ile Ile Ala Tyr Leu Met His Ser Asn Glu Gln Thr Leu Gln Arg Ser
 260 265 270
 Trp Ala Tyr Val Lys Lys Cys Lys Asn Asn Met Cys Pro Asn Arg Gly
 275 280 285
 Leu Val Ser Gln Leu Leu Glu Trp Glu Lys Thr Ile Leu Gly Asp Ser
 290 295 300
 Ile Thr Asn Ile Met Asp Pro Leu Tyr
 305 310

<210> 25

<211> 3440

<212> DNA

<213> Homo sapiens

<220>

<223> human metalloproteinase 1 (MP1) cDNA

<220>

<221> CDS

<222> (5)..(3118)

<223> MP1

<400> 25

cgcaatgtgg cgctgcggcg ggcggcgggg cctgtgtgtg ctgaggcggc tgagcggcgg 60

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gtataaacta	ggagacaaga	tccatggatt	caccgtaaac	caggtgacat	ctgttcccga	180
gctgttccctg	actgcagtga	agctcaccca	tgatgcacac	ggagccaggt	atttacacct	240
ggccagagaa	gacacgaata	atctgttccag	cgtgcagttc	cgtaccactc	ccatggacag	300
tactgggtgt	cctcacattc	ttgagcatac	cgtcctttgt	gggtctcaga	aatatccgtg	360
cagagaccct	ttcttcaaaa	tgttgaaccg	gtccctctcc	acgttcatga	acgccttcac	420
agctagtgat	tatactctgt	atccattttc	cacacaaaat	cccaaggact	ttcagaatct	480
cctctcggtg	tatttggtatg	ccaccttttt	cccattgttta	cgcgagctgg	atttctggca	540
ggaaggatgg	cggctggaac	atgagaatcc	gagcgacccc	cagacgccct	tggctcttaa	600
aggagtcgtc	tttaatgaga	tgaagggagc	gtttacagac	aatgagagga	tattctccca	660
gcaccttcag	aacagacttc	ttcccgaaca	cacgtactca	gtggtctccg	ggggtgacct	720
actgtgcatac	ccggagctta	catgggagca	gcttaagcag	tttcatgcca	ctcactatca	780
cccaagcaat	gctaggttct	tcacgtacgg	taattttcca	ttagaacagc	atctgaaaca	840
aattcacgag	gaagcactga	gcaaattcca	gaaaattgaa	ccaagcaccg	tggtgccagc	900
tcagacaccc	tgggacaagc	ctaggggaatt	ccagataaca	tgtggcccgg	attcatttgc	960
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cacatttgaa	gccttcacat	taagtcttct	gtcttcactc	ttgacttctg	ggcccaattc	1080
tccctttttac	aaagccttga	ttgaatctgg	ccttggcaca	gacttttctc	ctgatgttgg	1140
atataatggc	tacacgaggg	aggcctactt	tagtgtcggc	ctccaaggga	ttgtggagaa	1200
agacattgag	accgtcagaa	gcctcataga	cagaacgatt	gatgaagtag	ttgagaaagg	1260
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ggaaaatcca	aaatttttgc	aagaaaaagt	aaaacagtat	tttaagaata	accagcataa	1500
gctgacttta	tcgatgaggc	cagatgacaa	gtatcacgag	aagcaggcac	agggtggaagc	1560
cacgaagctc	aagcagaagg	tcgaggctct	gtcccccgga	gacaggcagc	agatctacga	1620
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agaattgaag	accggagggg	tgagtgtctc	tccccacgtg	ctccccgacg	actcacacat	1980
ggacacctac	gagcagggtg	tgcttttctc	ctctctctgc	ctggatcgaa	acctgccaga	2040
catgatgcag	ctatggagtg	aaatatttta	caaccctgtc	tttgaagaag	aggagcactt	2100
caaggtgctg	gtgaagatga	ccgcccagga	gctcgccaat	ggaattcctg	actctgggca	2160
cctgtacgca	tccatcaggg	caggccggac	cctcacgccc	gcaggggacc	tgcaggagac	2220
cttcagcggg	atggatcagg	tgcggtgat	gaagaggatt	gcagaaatga	cagatatcaa	2280
acctatcctg	aggaagctcc	cacgtatcaa	gaaacacttg	ttaaatggtg	ataatatgag	2340
gtgttcagtg	aatgcgactc	ctcagcagat	gcctcagaca	gaaaaagcgg	tcgaagactt	2400
ccttagaagc	atcggtcgga	gtaaaaagga	acggaggcct	gtgcgcccac	acacggtcga	2460
gaaacctgtg	cccagcagct	ctgggtggaga	tgcccacggt	ccccatggct	cccaggctcat	2520
taggaagctg	gtcatggaac	ccaccttcaa	gccctggcag	atgaagactc	acttctctgat	2580
gcccttcccg	gtgaattacg	tgggtgaatg	catccgaact	gtcccctaca	cggaccacga	2640
tcatgccagt	cttaaaatcc	ttgcacgttt	gatgactgcc	aaattcttgc	atacagaaat	2700
tcgagaaaaa	ggcggtgctt	atgggtggagg	cgcaaaaactc	agccacaatg	ggattttcac	2760
cctttactct	tacagggacc	caaatacaat	agagacgctc	cagtcttttg	ggaaggctgt	2820
cgactgggct	aagtctggaa	aattcacaca	gcaagacatc	gacgaagcca	aactttctgt	2880
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cggcctctcg	gatgagatga	agcaggccca	cagagagcag	ctctttgctg	tcagccacga	3000
caagctcctg	gccgtgagcg	ataggtacct	cggcactggg	aagagcacac	acggcctggc	3060
catcctcgga	cccagagaacc	cgaaaattgc	caaggaccca	tcttgatca	tccgatgagc	3120
agccgtggcg	ctcgactgca	caggagcccc	agacaataca	cctccgagct	gaatatgaaa	3180
agtcagaaat	gctactgctt	tttccaagaa	tattatgtca	ttgagtgtcg	ccaaagccct	3240
tgactggcga	gtcaaaaact	cagatctatc	ttaagagtga	ccaggaagag	gttcattgaa	3300
ataatcatgc	atgaagcgcc	aaagatgcac	catgtagaat	tttcaacttg	tactggcagg	3360
ctcgtttttac	ctcattctag	aatatttaag	aatctaaaaa	taaagggcaa	ctctgactta	3420
acaaaaaaaa	aaaaaaaaaa					3440

<210> 26
 <211> 1037
 <212> PRT
 <213> Homo sapiens

 <220>
 <223> human metalloproteinase 1 (MP1)

 <400> 26
 Met Trp Arg Cys Gly Gly Arg Arg Gly Leu Cys Val Leu Arg Arg Leu
 1 5 10 15
 Ser Gly Gly His Ala His His Arg Ala Trp Arg Trp Asn Ser Asn Arg
 20 25 30
 Ala Cys Glu Arg Ala Leu Gln Tyr Lys Leu Gly Asp Lys Ile His Gly
 35 40 45
 Phe Thr Val Asn Gln Val Thr Ser Val Pro Glu Leu Phe Leu Thr Ala
 50 55 60
 Val Lys Leu Thr His Asp Asp Thr Gly Ala Arg Tyr Leu His Leu Ala
 65 70 75 80
 Arg Glu Asp Thr Asn Asn Leu Phe Ser Val Gln Phe Arg Thr Thr Pro
 85 90 95
 Met Asp Ser Thr Gly Val Pro His Ile Leu Glu His Thr Val Leu Cys
 100 105 110
 Gly Ser Gln Lys Tyr Pro Cys Arg Asp Pro Phe Phe Lys Met Leu Asn
 115 120 125
 Arg Ser Leu Ser Thr Phe Met Asn Ala Phe Thr Ala Ser Asp Tyr Thr
 130 135 140
 Leu Tyr Pro Phe Ser Thr Gln Asn Pro Lys Asp Phe Gln Asn Leu Leu
 145 150 155 160
 Ser Val Tyr Leu Asp Ala Thr Phe Phe Pro Cys Leu Arg Glu Leu Asp
 165 170 175
 Phe Trp Gln Glu Gly Trp Arg Leu Glu His Glu Asn Pro Ser Asp Pro
 180 185 190
 Gln Thr Pro Leu Val Phe Lys Gly Val Val Phe Asn Glu Met Lys Gly
 195 200 205
 Ala Phe Thr Asp Asn Glu Arg Ile Phe Ser Gln His Leu Gln Asn Arg
 210 215 220
 Leu Leu Pro Asp His Thr Tyr Ser Val Val Ser Gly Gly Asp Pro Leu
 225 230 235 240
 Cys Ile Pro Glu Leu Thr Trp Glu Gln Leu Lys Gln Phe His Ala Thr
 245 250 255
 His Tyr His Pro Ser Asn Ala Arg Phe Phe Thr Tyr Gly Asn Phe Pro
 260 265 270

Leu	Glu	Gln	His	Leu	Lys	Gln	Ile	His	Glu	Glu	Ala	Leu	Ser	Lys	Phe	275	280	285
Gln	Lys	Ile	Glu	Pro	Ser	Thr	Val	Val	Pro	Ala	Gln	Thr	Pro	Trp	Asp	290	295	300
Lys	Pro	Arg	Glu	Phe	Gln	Ile	Thr	Cys	Gly	Pro	Asp	Ser	Phe	Ala	Thr	305	310	315
Asp	Pro	Ser	Lys	Gln	Thr	Thr	Val	Ser	Val	Ser	Phe	Leu	Leu	Pro	Asp	325	330	335
Ile	Thr	Asp	Thr	Phe	Glu	Ala	Phe	Thr	Leu	Ser	Leu	Leu	Ser	Ser	Leu	340	345	350
Leu	Thr	Ser	Gly	Pro	Asn	Ser	Pro	Phe	Tyr	Lys	Ala	Leu	Ile	Glu	Ser	355	360	365
Gly	Leu	Gly	Thr	Asp	Phe	Ser	Pro	Asp	Val	Gly	Tyr	Asn	Gly	Tyr	Thr	370	375	380
Arg	Glu	Ala	Tyr	Phe	Ser	Val	Gly	Leu	Gln	Gly	Ile	Val	Glu	Lys	Asp	385	390	395
Ile	Glu	Thr	Val	Arg	Ser	Leu	Ile	Asp	Arg	Thr	Ile	Asp	Glu	Val	Val	405	410	415
Glu	Lys	Gly	Phe	Glu	Asp	Asp	Arg	Ile	Glu	Ala	Leu	Leu	His	Lys	Ile	420	425	430
Glu	Ile	Gln	Met	Lys	His	Gln	Ser	Thr	Ser	Phe	Gly	Leu	Met	Leu	Thr	435	440	445
Ser	Tyr	Ile	Ala	Ser	Cys	Trp	Asn	His	Asp	Gly	Asp	Pro	Val	Glu	Leu	450	455	460
Leu	Lys	Leu	Gly	Asn	Gln	Leu	Ala	Lys	Phe	Arg	Gln	Cys	Leu	Gln	Glu	465	470	475
Asn	Pro	Lys	Phe	Leu	Gln	Glu	Lys	Val	Lys	Gln	Tyr	Phe	Lys	Asn	Asn	485	490	495
Gln	His	Lys	Leu	Thr	Leu	Ser	Met	Arg	Pro	Asp	Asp	Lys	Tyr	His	Glu	500	505	510
Lys	Gln	Ala	Gln	Val	Glu	Ala	Thr	Lys	Leu	Lys	Gln	Lys	Val	Glu	Ala	515	520	525
Leu	Ser	Pro	Gly	Asp	Arg	Gln	Gln	Ile	Tyr	Glu	Lys	Gly	Leu	Glu	Leu	530	535	540
Arg	Ser	Gln	Gln	Ser	Lys	Pro	Gln	Asp	Ala	Ser	Cys	Leu	Pro	Ala	Leu	545	550	555
Lys	Val	Ser	Asp	Ile	Glu	Pro	Thr	Ile	Pro	Val	Thr	Glu	Leu	Asp	Val	565	570	575
Val	Leu	Thr	Ala	Gly	Asp	Ile	Pro	Val	Gln	Tyr	Cys	Ala	Gln	Pro	Thr	580	585	590

Asn	Gly	Met	Val	Tyr	Phe	Arg	Ala	Phe	Ser	Ser	Leu	Asn	Thr	Leu	Pro	595	600	605
Glu	Glu	Leu	Arg	Pro	Tyr	Val	Pro	Leu	Phe	Cys	Ser	Val	Leu	Thr	Lys	610	615	620
Leu	Gly	Cys	Gly	Leu	Leu	Asp	Tyr	Arg	Glu	Gln	Ala	Gln	Gln	Ile	Glu	625	630	635
Leu	Lys	Thr	Gly	Gly	Met	Ser	Ala	Ser	Pro	His	Val	Leu	Pro	Asp	Asp	645	650	655
Ser	His	Met	Asp	Thr	Tyr	Glu	Gln	Gly	Val	Leu	Phe	Ser	Ser	Leu	Cys	660	665	670
Leu	Asp	Arg	Asn	Leu	Pro	Asp	Met	Met	Gln	Leu	Trp	Ser	Glu	Ile	Phe	675	680	685
Asn	Asn	Pro	Cys	Phe	Glu	Glu	Glu	Glu	His	Phe	Lys	Val	Leu	Val	Lys	690	695	700
Met	Thr	Ala	Gln	Glu	Leu	Ala	Asn	Gly	Ile	Pro	Asp	Ser	Gly	His	Leu	705	710	715
Tyr	Ala	Ser	Ile	Arg	Ala	Gly	Arg	Thr	Leu	Thr	Pro	Ala	Gly	Asp	Leu	725	730	735
Gln	Glu	Thr	Phe	Ser	Gly	Met	Asp	Gln	Val	Arg	Leu	Met	Lys	Arg	Ile	740	745	750
Ala	Glu	Met	Thr	Asp	Ile	Lys	Pro	Ile	Leu	Arg	Lys	Leu	Pro	Arg	Ile	755	760	765
Lys	Lys	His	Leu	Leu	Asn	Gly	Asp	Asn	Met	Arg	Cys	Ser	Val	Asn	Ala	770	775	780
Thr	Pro	Gln	Gln	Met	Pro	Gln	Thr	Glu	Lys	Ala	Val	Glu	Asp	Phe	Leu	785	790	795
Arg	Ser	Ile	Gly	Arg	Ser	Lys	Lys	Glu	Arg	Arg	Pro	Val	Arg	Pro	His	805	810	815
Thr	Val	Glu	Lys	Pro	Val	Pro	Ser	Ser	Ser	Gly	Gly	Asp	Ala	His	Val	820	825	830
Pro	His	Gly	Ser	Gln	Val	Ile	Arg	Lys	Leu	Val	Met	Glu	Pro	Thr	Phe	835	840	845
Lys	Pro	Trp	Gln	Met	Lys	Thr	His	Phe	Leu	Met	Pro	Phe	Pro	Val	Asn	850	855	860
Tyr	Val	Gly	Glu	Cys	Ile	Arg	Thr	Val	Pro	Tyr	Thr	Asp	Pro	Asp	His	865	870	875
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<213> Homo sapiens

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      (BPTF)

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Gln Asp Ser Glu Asp Asp Glu Glu Asp Glu Met Glu Glu Asp Asp Asp
      20                   25                   30

Asp Ser Asp Tyr Pro Glu Glu Met Glu Asp Asp Asp Asp Ala Ser
      35                   40                   45

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Tyr	Cys	Thr	Glu	Ser	Ser	Phe	Arg	Ser	His	Ser	Thr	Tyr	Ser	Ser	Thr	50	55	60
Pro	Gly	Arg	Arg	Lys	Pro	Arg	Val	His	Arg	Pro	Arg	Ser	Pro	Ile	Leu	65	70	75
Glu	Glu	Lys	Asp	Ile	Pro	Pro	Leu	Glu	Phe	Pro	Lys	Ser	Ser	Glu	Asp	85	90	95
Leu	Met	Val	Pro	Asn	Glu	His	Ile	Met	Asn	Val	Ile	Ala	Ile	Tyr	Glu	100	105	110
Val	Leu	Arg	Asn	Phe	Gly	Thr	Val	Leu	Arg	Leu	Ser	Pro	Phe	Arg	Phe	115	120	125
Glu	Asp	Phe	Cys	Ala	Ala	Leu	Val	Ser	Gln	Glu	Gln	Cys	Thr	Leu	Met	130	135	140
Ala	Glu	Met	His	Val	Val	Leu	Leu	Lys	Ala	Val	Leu	Arg	Glu	Glu	Asp	145	150	155
Thr	Ser	Asn	Thr	Thr	Phe	Gly	Pro	Ala	Asp	Leu	Lys	Asp	Ser	Val	Asn	165	170	175
Ser	Thr	Leu	Tyr	Phe	Ile	Asp	Gly	Met	Thr	Trp	Pro	Glu	Val	Leu	Arg	180	185	190
Val	Tyr	Cys	Glu	Ser	Asp	Lys	Glu	Tyr	His	His	Val	Leu	Pro	Tyr	Gln	195	200	205
Glu	Ala	Glu	Asp	Tyr	Pro	Tyr	Gly	Pro	Val	Glu	Asn	Lys	Ile	Lys	Val	210	215	220
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Pro	Ile	Gly	Tyr	Asp	Arg	Ser	Arg	Arg	Lys	Tyr	Trp	Phe	Leu	Asn	Arg	325	330	335
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Lys	Ala	Arg	Gly	Ser	Asn	Lys	Ser	Phe	Leu	Ala	Ala	Ala	Asn	Glu	Glu	405	410	415	
Ile	Leu	Glu	Ser	Ile	Arg	Ala	Lys	Lys	Gly	Asp	Ile	Asp	Asn	Val	Lys	420	425	430	
Ser	Pro	Glu	Glu	Thr	Glu	Lys	Asp	Lys	Asn	Glu	Thr	Glu	Asn	Asp	Ser	435	440	445	
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Lys	Asp	Ser	Asp	Asp	Lys	Thr	Pro	Asp	Asp	Asp	Pro	Glu	Gln	Gly	Lys	465	470	475	480
Ser	Glu	Val	Gly	Asp	Phe	Lys	Ser	Glu	Lys	Ser	Asn	Gly	Glu	Leu	Ser	485	490	495	
Glu	Ser	Pro	Gly	Ala	Gly	Lys	Gly	Ala	Ser	Gly	Ser	Thr	Arg	Ile	Ile	500	505	510	
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Lys	Glu	Val	Leu	Val	Val	Asn	Ser	Gln	Gly	Glu	Ile	Ser	Arg	Leu	Ser	545	550	555	560
Thr	Lys	Lys	Glu	Val	Ile	Met	Lys	Gly	Asn	Ile	Asn	Asn	Tyr	Phe	Lys	565	570	575	
Leu	Gly	Gln	Glu	Gly	Lys	Tyr	Arg	Val	Tyr	His	Asn	Gln	Tyr	Ser	Thr	580	585	590	
Asn	Ser	Phe	Ala	Leu	Asn	Lys	His	Gln	His	Arg	Glu	Asp	His	Asp	Lys	595	600	605	
Arg	Arg	His	Leu	Ala	His	Lys	Phe	Cys	Leu	Thr	Pro	Ala	Gly	Glu	Phe	610	615	620	
Lys	Trp	Asn	Gly	Ser	Val	His	Gly	Ser	Lys	Val	Leu	Thr	Ile	Ser	Thr	625	630	635	640
Leu	Arg	Leu	Thr	Ile	Thr	Gln	Leu	Glu	Asn	Asn	Ile	Pro	Ser	Ser	Phe	645	650	655	
Leu	His	Pro	Asn	Trp	Ala	Ser	His	Arg	Ala	Asn	Trp	Ile	Lys	Ala	Val	660	665	670	
Gln	Met	Cys	Ser	Lys	Pro	Arg	Glu	Phe	Ala	Leu	Ala	Leu	Ala	Ile	Leu	675	680	685	

44

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 1940 1945 1950
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 1955 1960 1965

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 2580 2585 2590
 Thr Ser Lys Glu Thr Lys Lys Asp Thr Lys Leu Tyr Cys Ile Cys Lys
 2595 2600 2605

Thr Pro Tyr Asp Glu Ser Lys Phe Tyr Ile Gly Cys Asp Arg Cys Gln
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 Asn Trp Tyr His Gly Arg Cys Val Gly Ile Leu Gln Ser Glu Ala Glu
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 Met Thr Val Leu Thr Pro Leu Thr Glu Lys Asp Tyr Glu Gly Leu Lys
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 Arg Val Leu Arg Ser Leu Gln Ala His Lys Met Ala Trp Pro Phe Leu
 2675 2680 2685
 Glu Pro Val Asp Pro Asn Asp Ala Pro Asp Tyr Tyr Gly Val Ile Lys
 2690 2695 2700
 Glu Pro Met Asp Leu Ala Thr Met Glu Glu Arg Val Gln Arg Arg Tyr
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 Tyr Glu Lys Leu Thr Glu Phe Val Ala Asp Met Thr Lys Ile Phe Asp
 2725 2730 2735
 Asn Cys Arg Tyr Tyr Asn Pro Ser Asp Ser Pro Phe Tyr Gln Cys Ala
 2740 2745 2750
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 2770 2775 2780

<210> 31
 <211> 2214
 <212> DNA
 <213> Mus musculus

<220>
 <223> mouse bromodomain PHD finger transcription factor
 (BPTF) partial cDNA

<220>
 <221> CDS
 <222> (2)..(1939)
 <223> BPTF (partial)

<400> 31
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 gtgtcagcct cagagcagtg tacaaggaca gtctcctgtt cgagtccaga gtccaccact 240
 gactcgaata tgtccatcaa ctccatccca agtgactcct ggacagcaac cccaggttca 300
 gactacagct tcacagccga ttccaattcc gccccccaca tctctgcagg caccttccca 360
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 gacattaaat caagttactg ttctatctcc atcctgtcct cagccacagc cccaagtcac 480
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 agttcagcaa aacagtgtctg cgcagactca gagtgtgggc acagtgcagg cagccagtg 660
 gcaggagcag ttgcagaggg ttcagcaact cagggaccag cagcaaaaga agaagcagca 720

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aacggacaaa ggaaaagcaa agtcaacggc accgttgtct tgtcgagagc aaatggcttt 2160
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<210> 32
<211> 645
<212> PRT
<213> Mus musculus

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<220>
<223> mouse bromodomain PHD finger transcription factor
      (BPTF), partial

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Thr Gln Pro Ala Val Ser Ser His Val Pro Ser Glu Thr Gln Pro Ser
      35              40              45

Gln Ala Gln Thr Ser Lys Pro Leu Val Ala Thr Gln Cys Gln Pro Gln
      50              55              60

Ser Ser Val Gln Gly Gln Ser Pro Val Arg Val Gln Ser Pro Pro Leu
      65              70              75              80

Thr Arg Ile Cys Pro Ser Thr Pro Ser Gln Val Thr Pro Gly Gln Gln
      85              90              95

Pro Gln Val Gln Thr Thr Ala Ser Gln Pro Ile Pro Ile Pro Pro Pro
      100             105             110

Thr Ser Leu Gln Ala Pro Ser Gln Gly Gln Pro Gln Ser Gln Pro Gln
      115             120             125

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Ala	Val	Pro	Gln	Leu	Gln	Gln	Val	Gln	Val	Leu	Ser	Gln	Ile	Gln	Ser	
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Gln	Val	Val	Ala	Gln	Ile	Gln	Ala	Gln	Gln	Ser	Gly	Val	Pro	Gln	Gln	
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Ile	Lys	Leu	Gln	Leu	Pro	Ile	Gln	Val	Gln	Gln	Asn	Ser	Ala	Ala	Gln	
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Thr	Gln	Ser	Val	Val	Thr	Val	Gln	Ala	Ala	Ser	Val	Gln	Glu	Gln	Leu	
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Ile	Glu	Thr	Glu	Arg	Glu	His	Thr	Leu	Gln	Ala	Ser	Asn	Gln	Ser	Glu	
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Ile	Ile	Gln	Lys	Gln	Val	Val	Met	Lys	His	Asn	Ala	Val	Ile	Glu	His	
			260					265					270			
Leu	Lys	Gln	Lys	Lys	Thr	Met	Thr	Pro	Ala	Glu	Arg	Glu	Glu	Asn	Gln	
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Arg	Met	Ile	Val	Cys	Asn	Gln	Val	Met	Lys	Tyr	Ile	Leu	Asp	Lys	Ile	
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Asp	Lys	Glu	Glu	Lys	Gln	Ala	Ala	Lys	Lys	Arg	Lys	Arg	Glu	Glu	Ser	
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Val	Glu	Gln	Lys	Arg	Ser	Lys	Gln	Asn	Ala	Ser	Lys	Leu	Ser	Ala	Leu	
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			340					345					350			
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Arg	Asp	Leu	Lys	Met	Lys	Arg	Glu	Arg	Glu	Met	Ala	Gln	Ala	Val	Gln	
	370					375					380					
Ala	Asn	Ala	Ala	Ser	Val	Pro	Thr	Pro	Ser	Val	Pro	Ala	Pro	Val	Pro	
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Ala	Pro	Ala	Pro	Ala	Ala	Pro	Pro	Ala	Pro	Pro	Arg	Ser	Pro	Pro	Pro	
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			420					425					430			
Val	Thr	Ser	Gln	Lys	Arg	Lys	Arg	Glu	Glu	Glu	Lys	Asp	Ser	Lys	Ser	
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Lys Lys Lys Lys Met Ile Ser Thr Thr Ser Lys Glu Ala Lys Lys Asp
 450 455 460
 Thr Arg Leu Tyr Cys Ile Cys Lys Thr Pro Tyr Asp Glu Ser Lys Phe
 465 470 475 480
 Tyr Ile Gly Cys Asp Arg Cys Gln Asn Trp Tyr His Gly Arg Cys Val
 485 490 495
 Gly Ile Leu Gln Ser Glu Ala Asp Leu Ile Asp Glu Tyr Val Cys Pro
 500 505 510
 Gln Cys Gln Ser Thr Glu Asp Ala Met Thr Val Leu Thr Pro Leu Thr
 515 520 525
 Glu Lys Asp Tyr Glu Gly Leu Lys Arg Val Leu Arg Ser Leu Gln Ala
 530 535 540
 His Lys Met Ala Trp Pro Phe Leu Glu Pro Val Asp Pro Asn Asp Ala
 545 550 555 560
 Pro Asp Tyr Tyr Gly Val Ile Lys Glu Pro Met Asp Leu Ala Thr Met
 565 570 575
 Glu Glu Arg Ile Gln Lys Arg Tyr Tyr Glu Lys Leu Thr Glu Phe Val
 580 585 590
 Ala Asp Met Thr Lys Ile Phe Asp Asn Cys Arg Tyr Tyr Asn Pro Arg
 595 600 605
 Asp Thr Pro Phe Tyr Gln Cys Ala Glu Val Leu Glu Ser Phe Phe Val
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 625 630 635 640
 Gln Ser Thr Ala Pro
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<210> 33

<211> 2156

<212> DNA

<213> Homo sapiens

<220>

<223> human tribbles homolog 2 (TRB2, GS3955) cDNA

<220>

<221> CDS

<222> (496)..(1527)

<223> GS3955

<400> 33

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 tcgcgtcggg agccctggcg ctgcagctcc gcaccttagc agcccgggta ctcattccaga 180
 tccacgccgg ggacacacac acagagtaac taaaagtgcg gcgattctgc acatcgccga 240
 ctgcttttgg gtaacaaaaa gacccgagtt gcctgcccgc cgaggacccc cgggagccgg 300
 gctcggagca gacgaggtat ccggcggcgc ccatttgggg gcttctaact ctttctccac 360
 gcagcccttc ttctgtcccc tcccctctcg ctccctttta aaatcagtgg caccgaggcg 420

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agccagagtt tcagcccga cctcgggtcc ccgagcccg ccgagactcc gaacttgtcg 660
cattgcgttt cttgtatcgg gaaatactta ttggtggaac ctctggaggg agaccacgtt 720
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<210> 34

<211> 343

<212> PRT

<213> Homo sapiens

<220>

<223> human tribbles homolog 2 (TRB2, GS3955)

<400> 34

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Ser Arg Asn Lys Thr Gln Asp Phe Glu Glu Leu Ser Ser Ile Arg Ser
20 25 30

Ala Glu Pro Ser Gln Ser Phe Ser Pro Asn Leu Gly Ser Pro Ser Pro
35 40 45

Pro Glu Thr Pro Asn Leu Ser His Cys Val Ser Cys Ile Gly Lys Tyr
50 55 60

Leu Leu Leu Glu Pro Leu Glu Gly Asp His Val Phe Arg Ala Val His
65 70 75 80

Leu His Ser Gly Glu Glu Leu Val Cys Lys Val Phe Asp Ile Ser Cys
85 90 95

Tyr Gln Glu Ser Leu Ala Pro Cys Phe Cys Leu Ser Ala His Ser Asn
100 105 110

Ile Asn Gln Ile Thr Glu Ile Ile Leu Gly Glu Thr Lys Ala Tyr Val
 115 120 125
 Phe Phe Glu Arg Ser Tyr Gly Asp Met His Ser Phe Val Arg Thr Cys
 130 135 140
 Lys Lys Leu Arg Glu Glu Glu Ala Ala Arg Leu Phe Tyr Gln Ile Ala
 145 150 155 160
 Ser Ala Val Ala His Cys His Asp Gly Gly Leu Val Leu Arg Asp Leu
 165 170 175
 Lys Leu Arg Lys Phe Ile Phe Lys Asp Glu Glu Arg Thr Arg Val Lys
 180 185 190
 Leu Glu Ser Leu Glu Asp Ala Tyr Ile Leu Arg Gly Asp Asp Asp Ser
 195 200 205
 Leu Ser Asp Lys His Gly Cys Pro Ala Tyr Val Ser Pro Glu Ile Leu
 210 215 220
 Asn Thr Ser Gly Ser Tyr Ser Gly Lys Ala Ala Asp Val Trp Ser Leu
 225 230 235 240
 Gly Val Met Leu Tyr Thr Met Leu Val Gly Arg Tyr Pro Phe His Asp
 245 250 255
 Ile Glu Pro Ser Ser Leu Phe Ser Lys Ile Arg Arg Gly Gln Phe Asn
 260 265 270
 Ile Pro Glu Thr Leu Ser Pro Lys Ala Lys Cys Leu Ile Arg Ser Ile
 275 280 285
 Leu Arg Arg Glu Pro Ser Glu Arg Leu Thr Ser Gln Glu Ile Leu Asp
 290 295 300
 His Pro Trp Phe Ser Thr Asp Phe Ser Val Ser Asn Ser Ala Tyr Gly
 305 310 315 320
 Ala Lys Glu Val Ser Asp Gln Leu Val Pro Asp Val Asn Met Glu Glu
 325 330 335
 Asn Leu Asp Pro Phe Phe Asn
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<210> 35
 <211> 3465
 <212> DNA
 <213> Mus musculus

<220>
 <223> mouse GS3955 cDNA

<220>
 <221> CDS
 <222> (555)..(1586)
 <223> GS3955

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tgccaac	aga	gacctga	gtccag	cgtg		agcttct	300
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cagacgg	gtc	ccctccc	ttc	ttgatc	cttt	gcctgc	480
gcgcgg	ctc	tccatct	ctc	cagagg	ggtt	ttgtcg	540
cgatcct	cac	actcat	gaac	atacac	aggt	agatat	600
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gctacc	agga	gtccc	tggcc	ccctg	cttct	atcaacc	900
tcacgga	aat	cctcct	ggga	gagacc	aaag	agctat	960
acatgc	attc	ctttgt	ccgc	acttg	taaga	gcccga	1020
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agaact	tgga	cccttt	cttt	aactg	agctc	aggtac	1620
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gaacac	gtag	catggg	aaaca	agacg	tgtgg	ggacgg	1800
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caggg	aaagg	acaatt	gatc	gaag	attttt	tggaac	2040
tgtaata	att	aataa	gattc	acct	aaaaat	cgggtg	2100
gaaacct	ggg	tgctaa	acta	aaaga	aaaaca	ttgtcg	2160
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gacacg	tgga	ctctag	tgtg	taaat	gtttac	ttga	3120
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 <211> 343
 <212> PRT
 <213> Mus musculus

<220>
 <223> mouse GS3955

<400> 36
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 Ala Glu Pro Ser Gln Ser Phe Ser Pro Asn Leu Gly Ser Pro Ser Pro
 35 40 45
 Pro Glu Thr Pro Asn Leu Ser His Cys Val Ser Cys Ile Gly Lys Tyr
 50 55 60
 Leu Leu Leu Glu Pro Leu Glu Gly Asp His Val Phe Arg Ala Val His
 65 70 75 80
 Leu His Ser Gly Glu Glu Leu Val Cys Lys Val Phe Glu Ile Ser Cys
 85 90 95
 Tyr Gln Glu Ser Leu Ala Pro Cys Phe Cys Leu Ser Ala His Ser Asn
 100 105 110
 Ile Asn Gln Ile Thr Glu Ile Leu Leu Gly Glu Thr Lys Ala Tyr Val
 115 120 125
 Phe Phe Glu Arg Ser Tyr Gly Asp Met His Ser Phe Val Arg Thr Cys
 130 135 140
 Lys Lys Leu Arg Glu Glu Glu Ala Ala Arg Leu Phe Tyr Gln Ile Ala
 145 150 155 160
 Ser Ala Val Ala His Cys His Asp Gly Gly Leu Val Leu Arg Asp Leu
 165 170 175
 Lys Leu Arg Lys Phe Ile Phe Lys Asp Glu Glu Arg Thr Arg Val Lys
 180 185 190
 Leu Glu Ser Leu Glu Asp Ala Tyr Ile Leu Arg Gly Asp Asp Asp Ser
 195 200 205
 Leu Ser Asp Lys His Gly Cys Pro Ala Tyr Val Ser Pro Glu Ile Leu
 210 215 220
 Asn Thr Ser Gly Ser Tyr Ser Gly Lys Ala Ala Asp Val Trp Ser Leu
 225 230 235 240
 Gly Val Met Leu Tyr Thr Met Leu Val Gly Arg Tyr Pro Phe His Asp
 245 250 255
 Ile Glu Pro Ser Ser Leu Phe Ser Lys Ile Arg Arg Gly Gln Phe Asn
 260 265 270

Ile Pro Glu Thr Leu Ser Pro Lys Ala Lys Cys Leu Ile Arg Ser Ile
 275 280 285
 Leu Arg Arg Glu Pro Ser Glu Arg Leu Thr Ser Gln Glu Ile Leu Asp
 290 295 300
 His Pro Trp Phe Ser Thr Asp Phe Ser Val Ser Asn Ser Gly Phe Gly
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 325 330 335
 Asn Leu Asp Pro Phe Phe Asn
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<210> 37
 <211> 2538
 <212> DNA
 <213> Homo sapiens

<220>
 <223> human follistatin-related protein (FRP) cDNA

<220>
 <221> CDS
 <222> (77)..(1003)
 <223> FRP

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<210> 38
<211> 308
<212> PRT
<213> Homo sapiens

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<220>
<223> human follistatin-related protein (FRP)

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Met Trp Lys Arg Trp Leu Ala Leu Ala Leu Ala Leu Val Ala Val Ala
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Trp Val Arg Ala Glu Glu Glu Leu Arg Ser Lys Ser Lys Ile Cys Ala
          20             25             30

Asn Val Phe Cys Gly Ala Gly Arg Glu Cys Ala Val Thr Glu Lys Gly
          35             40             45

Glu Pro Thr Cys Leu Cys Ile Glu Gln Cys Lys Pro His Lys Arg Pro
          50             55             60

Val Cys Gly Ser Asn Gly Lys Thr Tyr Leu Asn His Cys Glu Leu His
          65             70             75             80

Arg Asp Ala Cys Leu Thr Gly Ser Lys Ile Gln Val Asp Tyr Asp Gly
          85             90             95

His Cys Lys Glu Lys Lys Ser Val Ser Pro Ser Ala Ser Pro Val Val
          100            105            110

Cys Tyr Gln Ser Asn Arg Asp Glu Leu Arg Arg Arg Ile Ile Gln Trp
          115            120            125

Leu Glu Ala Glu Ile Ile Pro Asp Gly Trp Phe Ser Lys Gly Ser Asn
          130            135            140

Tyr Ser Glu Ile Leu Asp Lys Tyr Phe Lys Asn Phe Asp Asn Gly Asp
          145            150            155            160

Ser Arg Leu Asp Ser Ser Glu Phe Leu Lys Phe Val Glu Gln Asn Glu
          165            170            175

Thr Ala Ile Asn Ile Thr Thr Tyr Pro Asp Gln Glu Asn Asn Lys Leu
          180            185            190

Leu Arg Gly Leu Cys Val Asp Ala Leu Ile Glu Leu Ser Asp Glu Asn
          195            200            205

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Ala Asp Trp Lys Leu Ser Phe Gln Glu Phe Leu Lys Cys Leu Asn Pro
 210 215 220

Ser Phe Asn Pro Pro Glu Lys Lys Cys Ala Leu Glu Asp Glu Thr Tyr
 225 230 235 240

Ala Asp Gly Ala Glu Thr Glu Val Asp Cys Asn Arg Cys Val Cys Ala
 245 250 255

Cys Gly Asn Trp Val Cys Thr Ala Met Thr Cys Asp Gly Lys Asn Gln
 260 265 270

Lys Gly Ala Gln Thr Gln Thr Glu Glu Glu Met Thr Arg Tyr Val Gln
 275 280 285

Glu Leu Gln Lys His Gln Glu Thr Ala Glu Lys Thr Lys Arg Val Ser
 290 295 300

Thr Lys Glu Ile
 305

<210> 39
 <211> 2823
 <212> DNA
 <213> Mus musculus

<220>
 <223> mouse follistatin-like (Fstl),
 follistatin-related protein (FRP) cDNA

<220>
 <221> CDS
 <222> (80)..(1000)
 <223> FRP

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2823

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<210> 40
<211> 306
<212> PRT
<213> Mus musculus

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<220>
<223> mouse follistatin-like (Fst1),
      follistatin-related protein (FRP)

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<400> 40
Met Trp Lys Arg Trp Leu Ala Leu Ser Leu Val Thr Ile Ala Leu Val
 1             5             10            15

His Gly Glu Glu Glu Pro Arg Ser Lys Ser Lys Ile Cys Ala Asn Val
      20             25            30

Phe Cys Gly Ala Gly Arg Glu Cys Ala Val Thr Glu Lys Gly Glu Pro
      35             40            45

Thr Cys Leu Cys Ile Glu Gln Cys Lys Pro His Lys Arg Pro Val Cys
      50             55            60

Gly Ser Asn Gly Lys Thr Tyr Leu Asn His Cys Glu Leu His Arg Asp
      65             70            75            80

Ala Cys Leu Thr Gly Ser Lys Ile Gln Val Asp Tyr Asp Gly His Cys
      85             90            95

Lys Glu Lys Lys Ser Ala Ser Pro Ser Ala Ser Pro Val Val Cys Tyr
      100            105           110

Gln Ala Asn Arg Asp Glu Leu Arg Arg Arg Leu Ile Gln Trp Leu Glu
      115            120           125

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Ala Glu Ile Ile Pro Asp Gly Trp Phe Ser Lys Gly Ser Asn Tyr Ser
 130 135 140
 Glu Ile Leu Asp Lys Tyr Phe Lys Ser Phe Asp Asn Gly Asp Ser His
 145 150 155 160
 Leu Asp Ser Ser Glu Phe Leu Lys Phe Val Glu Gln Asn Glu Thr Ala
 165 170 175
 Ile Asn Ile Thr Thr Tyr Ala Asp Gln Glu Asn Asn Lys Leu Leu Arg
 180 185 190
 Ser Leu Cys Val Asp Ala Leu Ile Glu Leu Ser Asp Glu Asn Ala Asp
 195 200 205
 Trp Lys Leu Ser Phe Gln Glu Phe Leu Lys Cys Leu Asn Pro Ser Phe
 210 215 220
 Asn Pro Pro Glu Lys Lys Cys Ala Leu Glu Val Glu Thr Tyr Ala Asp
 225 230 235 240
 Gly Ala Glu Thr Glu Val Asp Cys Asn Arg Cys Val Cys Ser Cys Gly
 245 250 255
 His Trp Val Cys Thr Ala Met Thr Cys Asp Gly Lys Asn Gln Lys Gly
 260 265 270
 Val Gln Thr His Thr Glu Glu Glu Lys Thr Gly Tyr Val Gln Glu Leu
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 290 295 300
 Glu Ile
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<210> 41
 <211> 1370
 <212> DNA
 <213> Rattus norvegicus

<220>
 <223> rat follistatin-like (Fst1), follistatin-related
 protein (FRP) cDNA

<220>
 <221> CDS
 <222> (64)..(984)
 <223> FRP

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<210> 42
<211> 306
<212> PRT
<213> Rattus norvegicus

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<220>
<223> rat follistatin-like (Fst1), follistatin-related
        protein (FRP)

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<400> 42
Met Trp Lys Arg Trp Leu Ala Leu Ala Leu Val Thr Ile Ala Leu Val
  1               5               10               15

His Gly Glu Glu Glu Gln Arg Ser Lys Ser Lys Ile Cys Ala Asn Val
      20               25               30

Phe Cys Gly Ala Gly Arg Glu Cys Ala Val Thr Glu Lys Gly Glu Pro
      35               40               45

Thr Cys Leu Cys Ile Glu Gln Cys Lys Pro His Lys Arg Pro Val Cys
      50               55               60

Gly Ser Asn Gly Lys Thr Tyr Leu Asn His Cys Glu Leu His Arg Asp
      65               70               75               80

Ala Cys Leu Thr Gly Ser Lys Ile Gln Val Asp Tyr Asp Gly His Cys
      85               90               95

Lys Glu Lys Lys Ser Val Ser Pro Ser Ala Ser Pro Val Val Cys Tyr
      100              105              110

Gln Ala Asn Arg Asp Glu Leu Arg Arg Arg Ile Ile Gln Trp Leu Glu
      115              120              125

Ala Glu Ile Ile Pro Asp Gly Trp Phe Ser Lys Gly Ser Asn Tyr Ser
      130              135              140

Glu Ile Leu Asp Lys Tyr Phe Lys Ser Phe Asp Asn Gly Asp Ser His
      145              150              155              160

Leu Asp Ser Ser Glu Phe Leu Lys Phe Val Glu Gln Asn Glu Thr Ala
      165              170              175

Val Asn Ile Thr Ala Tyr Pro Asn Gln Glu Asn Asn Lys Leu Leu Arg
      180              185              190

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Gly Leu Cys Val Asp Ala Leu Ile Glu Leu Ser Asp Glu Asn Ala Asp
 195 200 205
 Trp Lys Leu Ser Phe Gln Glu Phe Leu Lys Cys Leu Asn Pro Ser Phe
 210 215 220
 Asn Pro Pro Glu Lys Lys Cys Ala Leu Glu Asp Glu Thr Tyr Ala Asp
 225 230 235 240
 Gly Ala Glu Thr Glu Val Asp Cys Asn Arg Cys Val Cys Ser Cys Gly
 245 250 255
 His Trp Val Cys Thr Ala Met Thr Cys Asp Gly Lys Asn Gln Lys Gly
 260 265 270
 Val Gln Thr His Thr Glu Glu Glu Met Thr Arg Tyr Ala Gln Glu Leu
 275 280 285
 Gln Lys His Gln Gly Thr Ala Glu Lys Thr Lys Lys Val Asn Thr Lys
 290 295 300
 Glu Ile
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<210> 43
 <211> 2532
 <212> DNA
 <213> Homo sapiens

<220>
 <223> human alcohol dehydrogenase (ADH2) cDNA

<220>
 <221> CDS
 <222> (73)..(1200)
 <223> ADH2

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 aacctggtga ccccccttcc tgtgatttta ggccatgagg cagccggcat cgtggagagt 300
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aatagtttat ca 2532

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<210> 44
<211> 375
<212> PRT
<213> Homo sapiens

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<220>
<223> human alcohol dehydrogenase (ADH2)

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Met Ser Thr Ala Gly Lys Val Ile Lys Cys Lys Ala Ala Val Leu Trp
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Glu Val Lys Lys Pro Phe Ser Ile Glu Asp Val Glu Val Ala Pro Pro
          20             25             30

Lys Ala Tyr Glu Val Arg Ile Lys Met Val Ala Val Gly Ile Cys Arg
          35             40             45

Thr Asp Asp His Val Val Ser Gly Asn Leu Val Thr Pro Leu Pro Val
          50             55             60

Ile Leu Gly His Glu Ala Ala Gly Ile Val Glu Ser Val Gly Glu Gly
          65             70             75             80

Val Thr Thr Val Lys Pro Gly Asp Lys Val Ile Pro Leu Phe Thr Pro
          85             90             95

Gln Cys Gly Lys Cys Arg Val Cys Lys Asn Pro Glu Ser Asn Tyr Cys
          100            105            110

Leu Lys Asn Asp Leu Gly Asn Pro Arg Gly Thr Leu Gln Asp Gly Thr
          115            120            125

Arg Arg Phe Thr Cys Arg Gly Lys Pro Ile His His Phe Leu Gly Thr
          130            135            140

Ser Thr Phe Ser Gln Tyr Thr Val Val Asp Glu Asn Ala Val Ala Lys
          145            150            155            160

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Ile Asp Ala Ala Ser Pro Leu Glu Lys Val Cys Leu Ile Gly Cys Gly
 165 170 175
 Phe Ser Thr Gly Tyr Gly Ser Ala Val Asn Val Ala Lys Val Thr Pro
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 Gly Ser Thr Cys Ala Val Phe Gly Leu Gly Gly Val Gly Leu Ser Ala
 195 200 205
 Val Met Gly Cys Lys Ala Ala Gly Ala Ala Arg Ile Ile Ala Val Asp
 210 215 220
 Ile Asn Lys Asp Lys Phe Ala Lys Ala Lys Glu Leu Gly Ala Thr Glu
 225 230 235 240
 Cys Ile Asn Pro Gln Asp Tyr Lys Lys Pro Ile Gln Glu Val Leu Lys
 245 250 255
 Glu Met Thr Asp Gly Gly Val Asp Phe Ser Phe Glu Val Ile Gly Arg
 260 265 270
 Leu Asp Thr Met Met Ala Ser Leu Leu Cys Cys His Glu Ala Cys Gly
 275 280 285
 Thr Ser Val Ile Val Gly Val Pro Pro Ala Ser Gln Asn Leu Ser Ile
 290 295 300
 Asn Pro Met Leu Leu Leu Thr Gly Arg Thr Trp Lys Gly Ala Val Tyr
 305 310 315 320
 Gly Gly Phe Lys Ser Lys Glu Gly Ile Pro Lys Leu Val Ala Asp Phe
 325 330 335
 Met Ala Lys Lys Phe Ser Leu Asp Ala Leu Ile Thr His Val Leu Pro
 340 345 350
 Phe Glu Lys Ile Asn Glu Gly Phe Asp Leu Leu His Ser Gly Lys Ser
 355 360 365
 Ile Arg Thr Val Leu Thr Phe
 370 375

<210> 45

<211> 1128

<212> DNA

<213> Mus musculus

<220>

<223> mouse alcohol dehydrogenase (ADH2) cDNA

<220>

<221> CDS

<222> (1)..(1128)

<223> ADH2

<400> 45

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 atggtggcca ctggtgtctg ccgctcagac gatcacgtgg ttagtggaa cctggtcaca 180
 cctcttctctg cagtttttagg ccatgaggga gcaggcattg ttgagagcgt tggagaaggg 240

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gtgacttggtg tgaaccagg tgataaagtc attccactct tttccctca gtgtggagaa 300
tgcaggattt gcaagcacc ggaaagcaac tttttagacc gaagcgatct gctaatacct 360
cgggggactt tgcgcgaagg caccagcagg ttctcctgca agggaaagca gatccacaac 420
tttatcagca ccagcacctt ctcccagtag accgtggtag atgatatagc agtggccaaa 480
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ctcggagggtg tcggtctgtc tgtcatcatt ggctgtaaag cagcaggagc agccaggatc 660
attgctgtgg acatcaacaa ggacaagttt gccaaaggcca aagagttggg tgcaactgag 720
tgcatacaacc ctcaagacta cagcaaacc atccaggaag ttctccagga gatgaccgac 780
ggaggggtgg acttttcggt tgaagtcac ggccgccttg acaccatgac ttctgccctg 840
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tttcggttg acccgtaaat tacccatgtt ttaccttcg agaaaataaa tgaagcattt 1080
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<210> 46
 <211> 375
 <212> PRT
 <213> Mus musculus

<220>
 <223> mouse alcohol dehydrogenase (ADH2)

<400> 46
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 Glu Leu His Lys Pro Phe Thr Ile Glu Asp Ile Glu Val Ala Pro Pro
 20 25 30
 Lys Ala His Glu Val Arg Ile Lys Met Val Ala Thr Gly Val Cys Arg
 35 40 45
 Ser Asp Asp His Val Val Ser Gly Thr Leu Val Thr Pro Leu Pro Ala
 50 55 60
 Val Leu Gly His Glu Gly Ala Gly Ile Val Glu Ser Val Gly Glu Gly
 65 70 75 80
 Val Thr Cys Val Lys Pro Gly Asp Lys Val Ile Pro Leu Phe Ser Pro
 85 90 95
 Gln Cys Gly Glu Cys Arg Ile Cys Lys His Pro Glu Ser Asn Phe Cys
 100 105 110
 Ser Arg Ser Asp Leu Leu Met Pro Arg Gly Thr Leu Arg Glu Gly Thr
 115 120 125
 Ser Arg Phe Ser Cys Lys Gly Lys Gln Ile His Asn Phe Ile Ser Thr
 130 135 140
 Ser Thr Phe Ser Gln Tyr Thr Val Val Asp Asp Ile Ala Val Ala Lys
 145 150 155 160
 Ile Asp Gly Ala Ser Pro Leu Asp Lys Val Cys Leu Ile Gly Cys Gly
 165 170 175
 Phe Ser Thr Gly Tyr Gly Ser Ala Val Lys Val Ala Lys Val Thr Pro
 180 185 190

Gly Ser Thr Cys Ala Val Phe Gly Leu Gly Gly Val Gly Leu Ser Val
 195 200 205
 Ile Ile Gly Cys Lys Ala Ala Gly Ala Ala Arg Ile Ile Ala Val Asp
 210 215 220
 Ile Asn Lys Asp Lys Phe Ala Lys Ala Lys Glu Leu Gly Ala Thr Glu
 225 230 235 240
 Cys Ile Asn Pro Gln Asp Tyr Ser Lys Pro Ile Gln Glu Val Leu Gln
 245 250 255
 Glu Met Thr Asp Gly Gly Val Asp Phe Ser Phe Glu Val Ile Gly Arg
 260 265 270
 Leu Asp Thr Met Thr Ser Ala Leu Leu Ser Cys His Ala Ala Cys Gly
 275 280 285
 Val Ser Val Val Val Gly Val Pro Pro Asn Ala Gln Asn Leu Ser Met
 290 295 300
 Asn Pro Met Leu Leu Leu Leu Gly Arg Thr Trp Lys Gly Ala Ile Phe
 305 310 315 320
 Gly Gly Phe Lys Ser Lys Asp Ser Val Pro Lys Leu Val Ala Asp Phe
 325 330 335
 Met Ala Lys Lys Phe Pro Leu Asp Pro Leu Ile Thr His Val Leu Pro
 340 345 350
 Phe Glu Lys Ile Asn Glu Ala Phe Asp Leu Leu Arg Ser Gly Lys Ser
 355 360 365
 Ile Arg Thr Val Leu Thr Phe
 370 375

<210> 47
 <211> 1131
 <212> DNA
 <213> Rattus norvegicus

<220>
 <223> rat alcohol dehydrogenase (ADH2) cDNA

<220>
 <221> CDS
 <222> (1)..(1131)
 <223> ADH2

<400> 47
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 atggtggcca ccggagtcctg ccgctcagac gatcacgcgg ttagtggatc cctgttcacg 180
 cctcttctctg cagttctagg ccacgagggg gctggcattg ttgagagcat tggagaaggg 240
 gtgacttggtg tgaaaccagg tgataaagtc atcccgtgtg tctctcccca gtgtggaaaa 300
 tgcaggatct gcaagcaccg ggaagcaac ctctgttgcc aaactaagaa tctgacacag 360
 cctaaggag ctttgctgga cggcaccagc aggttctcct gcaggggaaa gccattcac 420
 cacttcatca gcaccagcac cttctccag tacactgtgg tagatgacat agcgggtggcc 480
 aaaatcgatg cggctgcacc gctggacaaa gtctgcctca tcggctgtgg cttctcgact 540
 ggctatggct ctgccgtcca agtcgccaaag gtgaccccag gctccacctg tgccgtgttt 600

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ggcctgggag gtgttgggtct gtctgtcgtc attggctgta aaacagcagg agcagccaag 660
atcattgccc tggacatcaa caaagacaag tttgcgaagg ccaaagagtt aggtgccact 720
gactgtatca accctcaaga ctacaccaa cccatccagg aagttctcca ggagatgact 780
gatggagggg tggacttttc atttgaagtc attggccgtc ttgataccat gacttctgcc 840
ctgttaagct gccattcagc atgcggtgta agcgtcattg tcgggggtgcc tcccagtgcc 900
caaagcctct ccgttaaccc catgtcgtcg ctgctgggac gcacctggaa aggagcaata 960
ttcggcgggt ttaagagtaa agatgccgtc cccaaacttg tcgctgactt catggctaag 1020
aagtttccgt tggagccgct gattactcat gttttacctt ttgaaaagat aaatgaagca 1080
tttgacctgc tccgtgctgg aaagagtatc cgtaccgtcc tgacgttctg a 1131

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<210> 48
 <211> 376
 <212> PRT
 <213> Rattus norvegicus

<220>
 <223> rat alcohol dehydrogenase (ADH2)

<400> 48
 Met Ser Thr Ala Gly Lys Val Ile Lys Cys Lys Ala Ala Val Leu Trp
 1 5 10 15
 Glu Pro His Lys Pro Phe Thr Ile Glu Asp Ile Glu Val Ala Pro Pro
 20 25 30
 Lys Ala His Glu Val Arg Ile Lys Met Val Ala Thr Gly Val Cys Arg
 35 40 45
 Ser Asp Asp His Ala Val Ser Gly Ser Leu Phe Thr Pro Leu Pro Ala
 50 55 60
 Val Leu Gly His Glu Gly Ala Gly Ile Val Glu Ser Ile Gly Glu Gly
 65 70 75 80
 Val Thr Cys Val Lys Pro Gly Asp Lys Val Ile Pro Leu Phe Ser Pro
 85 90 95
 Gln Cys Gly Lys Cys Arg Ile Cys Lys His Pro Glu Ser Asn Leu Cys
 100 105 110
 Cys Gln Thr Lys Asn Leu Thr Gln Pro Lys Gly Ala Leu Leu Asp Gly
 115 120 125
 Thr Ser Arg Phe Ser Cys Arg Gly Lys Pro Ile His His Phe Ile Ser
 130 135 140
 Thr Ser Thr Phe Ser Gln Tyr Thr Val Val Asp Asp Ile Ala Val Ala
 145 150 155 160
 Lys Ile Asp Ala Ala Ala Pro Leu Asp Lys Val Cys Leu Ile Gly Cys
 165 170 175
 Gly Phe Ser Thr Gly Tyr Gly Ser Ala Val Gln Val Ala Lys Val Thr
 180 185 190
 Pro Gly Ser Thr Cys Ala Val Phe Gly Leu Gly Gly Val Gly Leu Ser
 195 200 205
 Val Val Ile Gly Cys Lys Thr Ala Gly Ala Ala Lys Ile Ile Ala Val
 210 215 220

Asp Ile Asn Lys Asp Lys Phe Ala Lys Ala Lys Glu Leu Gly Ala Thr
 225 230 235 240
 Asp Cys Ile Asn Pro Gln Asp Tyr Thr Lys Pro Ile Gln Glu Val Leu
 245 250 255
 Gln Glu Met Thr Asp Gly Gly Val Asp Phe Ser Phe Glu Val Ile Gly
 260 265 270
 Arg Leu Asp Thr Met Thr Ser Ala Leu Leu Ser Cys His Ser Ala Cys
 275 280 285
 Gly Val Ser Val Ile Val Gly Val Pro Pro Ser Ala Gln Ser Leu Ser
 290 295 300
 Val Asn Pro Met Ser Leu Leu Leu Gly Arg Thr Trp Lys Gly Ala Ile
 305 310 315 320
 Phe Gly Gly Phe Lys Ser Lys Asp Ala Val Pro Lys Leu Val Ala Asp
 325 330 335
 Phe Met Ala Lys Lys Phe Pro Leu Glu Pro Leu Ile Thr His Val Leu
 340 345 350
 Pro Phe Glu Lys Ile Asn Glu Ala Phe Asp Leu Leu Arg Ala Gly Lys
 355 360 365
 Ser Ile Arg Thr Val Leu Thr Phe
 370 375

<210> 49

<211> 582

<212> DNA

<213> Homo sapiens

<220>

<223> human acylphosphatase, erythrocyte isoenzyme cDNA

<220>

<221> CDS

<222> (69)..(368)

<223> acylphosphatase

<220>

<221> modified_base

<222> (582)

<223> n = g, a, c or t

<400> 49

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tgcaaggggt gtttttccgt aagcatactc aggctgaggg taaaaagctg ggattggtag 180
gctgggtcca gaacactgac cggggcacag tgcaaggaca attgcaaggt ccaatctcca 240
aggtgcggtca tatgcaggaa tggcttgaaa caagaggaag tcctaaatca cacatcgaca 300
aagcaaactt caacaatgaa aaagtcattt tgaagttgga ttactcagac ttccaaattg 360
taaaataatg gcctgaattt aagttttcta agataaactc agtggtttgg tttttattat 420
taatagagat agaactattg tgtgttaata ttagcattag tcaataagtt attttaatgt 480
cagatttttg aatgttatat atattacctg tatgatggaa ggattaccac tgtacacaaa 540
tctaataaat aaaaacgtta gaaccttctg cttagagtac an 582

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<210> 50
 <211> 99
 <212> PRT
 <213> Homo sapiens

 <220>
 <223> human acylphosphatase, erythrocyte isoenzyme

 <400> 50
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 1 5 10 15
 Lys Val Gln Gly Val Phe Phe Arg Lys His Thr Gln Ala Glu Gly Lys
 20 25 30
 Lys Leu Gly Leu Val Gly Trp Val Gln Asn Thr Asp Arg Gly Thr Val
 35 40 45
 Gln Gly Gln Leu Gln Gly Pro Ile Ser Lys Val Arg His Met Gln Glu
 50 55 60
 Trp Leu Glu Thr Arg Gly Ser Pro Lys Ser His Ile Asp Lys Ala Asn
 65 70 75 80
 Phe Asn Asn Glu Lys Val Ile Leu Lys Leu Asp Tyr Ser Asp Phe Gln
 85 90 95

 Ile Val Lys

<210> 51
 <211> 640
 <212> DNA
 <213> Mus musculus

 <220>
 <223> mouse acylphosphatase, erythrocyte isoenzyme cDNA

 <220>
 <221> CDS
 <222> (135)..(434)
 <223> acylphosphatase

<400> 51
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 ccaagtgttt gagcatggca gaaggggaca ccttggtctc agtggattac gaaatttttg 180
 gaaagggttca aggggtgttt ttccgcaagt acactcaggc tgagggtaaa aagctagggt 240
 tgggtgggctg gggttcagaac accgaccggg gcaccgtgca agggcaactg cagggccccg 300
 tctccaagggt gcgcttcatg cagcagtggc tggagaccag aggaagtccc aagtcgcaca 360
 ttgacagagc aaacttcaac aatgagaaag tcatcgcaaa cttggattat tcagacttcc 420
 aaattgtaaa ataatgaaac gaatcttaat attttttcaa aataatctca ctcctttttt 480
 taaatcgcta gattaaaaaa aaaatagaac tattctgtgc tcagtattag aatttggttag 540
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 aatgtgtata attctaacca ataaaaacac attagaacct 640

<210> 52
 <211> 99
 <212> PRT
 <213> Mus musculus

 <220>
 <223> mouse acylphosphatase, erythrocyte isoenzyme

 <400> 52
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 1 5 10 15
 Lys Val Gln Gly Val Phe Phe Arg Lys Tyr Thr Gln Ala Glu Gly Lys
 20 25 30
 Lys Leu Gly Leu Val Gly Trp Val Gln Asn Thr Asp Arg Gly Thr Val
 35 40 45
 Gln Gly Gln Leu Gln Gly Pro Val Ser Lys Val Arg Phe Met Gln Gln
 50 55 60
 Trp Leu Glu Thr Arg Gly Ser Pro Lys Ser His Ile Asp Arg Ala Asn
 65 70 75 80
 Phe Asn Asn Glu Lys Val Ile Ala Asn Leu Asp Tyr Ser Asp Phe Gln
 85 90 95

 Ile Val Lys

<210> 53
 <211> 2968
 <212> DNA
 <213> Homo sapiens

 <220>
 <223> human protein-kinase C-related kinase 1 (PRK1,
 PKN) cDNA

 <220>
 <221> CDS
 <222> (37)..(2865)
 <223> PRK1

 <400> 53
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 gagctgaagc tgaaggaggg tgctgagaac ctgcggcggg ccaccactga cctgggccgc 240
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 gcgggcctgg agaagcagtt ggccattgag ctgaagggtga agcagggggc ggagaacatg 480
 atccagacct acagcaatgg cagcaccaag gaccggaagc tgctgctgac agcccagcag 540
 atgttgcaag acagtaagac caagattgac atcatccgca tgcaactccg ccgggcgctg 600
 caggccggcc agctggagaa ccaggcagcc ccggatgaca cccaaggagg tcctgacctg 660
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aaaaaaaaaa aaaaaaaaaa aggaattc 2968

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<210> 54
 <211> 942
 <212> PRT
 <213> Homo sapiens

<220>
 <223> human protein-kinase C-related kinase 1 (PRK1,
 PKN)

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 20 25 30
 Gln Gln Leu Glu Leu Glu Arg Glu Arg Leu Arg Arg Glu Ile Arg Lys
 35 40 45
 Glu Leu Lys Leu Lys Glu Gly Ala Glu Asn Leu Arg Arg Ala Thr Thr
 50 55 60
 Asp Leu Gly Arg Ser Leu Gly Pro Val Glu Leu Leu Leu Arg Gly Ser
 65 70 75 80

Ser Arg Arg Leu Asp Leu Leu His Gln Gln Leu Gln Glu Leu His Ala
 85 90 95
 His Val Val Leu Pro Asp Pro Ala Ala Thr His Asp Gly Pro Gln Ser
 100 105 110
 Pro Gly Ala Gly Gly Pro Thr Cys Ser Ala Thr Asn Leu Ser Arg Val
 115 120 125
 Ala Gly Leu Glu Lys Gln Leu Ala Ile Glu Leu Lys Val Lys Gln Gly
 130 135 140
 Ala Glu Asn Met Ile Gln Thr Tyr Ser Asn Gly Ser Thr Lys Asp Arg
 145 150 155 160
 Lys Leu Leu Leu Thr Ala Gln Gln Met Leu Gln Asp Ser Lys Thr Lys
 165 170 175
 Ile Asp Ile Ile Arg Met Gln Leu Arg Arg Ala Leu Gln Ala Gly Gln
 180 185 190
 Leu Glu Asn Gln Ala Ala Pro Asp Asp Thr Gln Gly Ser Pro Asp Leu
 195 200 205
 Gly Ala Val Glu Leu Arg Ile Glu Glu Leu Arg His His Phe Arg Val
 210 215 220
 Glu His Ala Val Ala Glu Gly Ala Lys Asn Val Leu Arg Leu Leu Ser
 225 230 235 240
 Ala Ala Lys Ala Pro Asp Arg Lys Ala Val Ser Glu Ala Gln Glu Lys
 245 250 255
 Leu Thr Glu Ser Asn Gln Lys Leu Gly Leu Leu Arg Glu Ala Leu Glu
 260 265 270
 Arg Arg Leu Gly Glu Leu Pro Ala Asp His Pro Lys Gly Arg Leu Leu
 275 280 285
 Arg Glu Glu Leu Ala Ala Ala Ser Ser Ala Ala Phe Ser Thr Arg Leu
 290 295 300
 Ala Gly Pro Phe Pro Ala Thr His Tyr Ser Thr Leu Cys Lys Pro Ala
 305 310 315 320
 Pro Leu Thr Gly Thr Leu Glu Val Arg Val Val Gly Cys Arg Asp Leu
 325 330 335
 Pro Glu Thr Ile Pro Trp Asn Pro Thr Pro Ser Met Gly Gly Pro Gly
 340 345 350
 Thr Pro Asp Ser Arg Pro Pro Phe Leu Ser Arg Pro Ala Arg Gly Leu
 355 360 365
 Tyr Ser Arg Ser Gly Ser Leu Ser Gly Arg Ser Ser Leu Lys Ala Glu
 370 375 380
 Ala Glu Asn Thr Ser Glu Val Ser Thr Val Leu Lys Leu Asp Asn Thr
 385 390 395 400

Val	Val	Gly	Gln	Thr	Ser	Trp	Lys	Pro	Cys	Gly	Pro	Asn	Ala	Trp	Asp	
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Gln	Ser	Phe	Thr	Leu	Glu	Leu	Glu	Arg	Ala	Arg	Glu	Leu	Glu	Leu	Ala	
			420					425					430			
Val	Phe	Trp	Arg	Asp	Gln	Arg	Gly	Leu	Cys	Ala	Leu	Lys	Phe	Leu	Lys	
		435					440					445				
Leu	Glu	Asp	Phe	Leu	Asp	Asn	Glu	Arg	His	Glu	Val	Gln	Leu	Asp	Met	
	450					455					460					
Glu	Pro	Gln	Gly	Cys	Leu	Val	Ala	Glu	Val	Thr	Phe	Arg	Asn	Pro	Val	
465					470					475					480	
Ile	Glu	Arg	Ile	Pro	Arg	Leu	Arg	Arg	Gln	Lys	Lys	Ile	Phe	Ser	Lys	
				485					490					495		
Gln	Gln	Gly	Lys	Ala	Phe	Gln	Arg	Ala	Arg	Gln	Met	Asn	Ile	Asp	Val	
			500					505					510			
Ala	Thr	Trp	Val	Arg	Leu	Leu	Arg	Arg	Leu	Ile	Pro	Asn	Ala	Thr	Gly	
		515					520						525			
Thr	Gly	Thr	Phe	Ser	Pro	Gly	Ala	Ser	Pro	Gly	Ser	Glu	Ala	Arg	Thr	
	530					535					540					
Thr	Gly	Asp	Ile	Ser	Val	Glu	Lys	Leu	Asn	Leu	Gly	Thr	Asp	Ser	Asp	
545					550					555					560	
Ser	Ser	Pro	Gln	Lys	Ser	Ser	Arg	Asp	Pro	Pro	Ser	Ser	Pro	Ser	Ser	
				565					570					575		
Leu	Ser	Ser	Pro	Ile	Gln	Glu	Ser	Thr	Ala	Pro	Glu	Leu	Pro	Ser	Glu	
			580					585					590			
Thr	Gln	Glu	Thr	Pro	Gly	Pro	Ala	Leu	Cys	Ser	Pro	Leu	Arg	Lys	Ser	
		595					600					605				
Pro	Leu	Thr	Leu	Glu	Asp	Phe	Lys	Phe	Leu	Ala	Val	Leu	Gly	Arg	Gly	
	610					615					620					
His	Phe	Gly	Lys	Val	Leu	Leu	Ser	Glu	Phe	Arg	Pro	Ser	Gly	Glu	Leu	
625					630					635					640	
Phe	Ala	Ile	Lys	Ala	Leu	Lys	Lys	Gly	Asp	Ile	Val	Ala	Arg	Asp	Glu	
				645					650					655		
Val	Glu	Ser	Leu	Met	Cys	Glu	Lys	Arg	Ile	Leu	Ala	Ala	Val	Thr	Ser	
			660					665					670			
Ala	Gly	His	Pro	Phe	Leu	Val	Asn	Leu	Phe	Gly	Cys	Phe	Gln	Thr	Pro	
		675					680					685				
Glu	His	Val	Cys	Phe	Val	Met	Glu	Tyr	Ser	Ala	Gly	Gly	Asp	Leu	Met	
	690					695					700					
Leu	His	Ile	His	Ser	Asp	Val	Phe	Ser	Glu	Pro	Arg	Ala	Ile	Phe	Tyr	
705					710					715					720	

Ser Ala Cys Val Val Leu Gly Leu Gln Phe Leu His Glu His Lys Ile
 725 730 735
 Val Tyr Arg Asp Leu Lys Leu Asp Asn Leu Leu Leu Asp Thr Glu Gly
 740 745 750
 Tyr Val Lys Ile Ala Asp Phe Gly Leu Cys Lys Glu Gly Met Gly Tyr
 755 760 765
 Gly Asp Arg Thr Ser Thr Phe Cys Gly Thr Pro Glu Phe Leu Ala Pro
 770 775 780
 Glu Val Leu Thr Asp Thr Ser Tyr Thr Arg Ala Val Asp Trp Trp Gly
 785 790 795 800
 Leu Gly Val Leu Leu Tyr Glu Met Leu Val Gly Glu Ser Pro Phe Pro
 805 810 815
 Gly Asp Asp Glu Glu Glu Val Phe Asp Ser Ile Val Asn Asp Glu Val
 820 825 830
 Arg Tyr Pro Arg Phe Leu Ser Ala Glu Ala Ile Gly Ile Met Arg Arg
 835 840 845
 Leu Leu Arg Arg Asn Pro Glu Arg Arg Leu Gly Ser Ser Glu Arg Asp
 850 855 860
 Ala Glu Asp Val Lys Lys Gln Pro Phe Phe Arg Thr Leu Gly Trp Glu
 865 870 875 880
 Ala Leu Leu Ala Arg Arg Leu Pro Pro Pro Phe Val Pro Thr Leu Ser
 885 890 895
 Gly Arg Thr Asp Val Ser Asn Phe Asp Glu Glu Phe Thr Gly Glu Ala
 900 905 910
 Pro Thr Leu Ser Pro Pro Arg Asp Ala Arg Pro Leu Thr Ala Ala Glu
 915 920 925
 Gln Ala Ala Phe Leu Asp Phe Asp Phe Val Ala Gly Gly Cys
 930 935 940

<210> 55

<211> 1193

<212> DNA

<213> Mus musculus

<220>

<223> mouse protein-kinase C-related kinase 1 (PRK1),
 protein-kinase C-like 1, serine/threonine protein
 kinase N (PKN) cDNA

<220>

<221> CDS

<222> (229)..(1077)

<223> PRK1

<400> 55

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cggatttttg cggccgtgac cagggcagga catcccttcc tgggtgaacct tttcggtgtg 300
ttccagacct cagagcacgt gtgctttgtg atggagtact cggcgggtgg agacctgatg 360
ctgcacattc atagcgacgt gttctcagag cctcgggtg tcttctattc ggcctgtgtg 420
gtgctgggac tgcagttcct ccatgaacac aagattgtct acagggacct gaagttggac 480
aatttgctcc tggatactga gggctacgtc aagatcgag actttggcct ctgcaaggag 540
gggatgggct atggggaccg gaccagcacg ttctgcggaa ctccggagtt cctggcgccg 600
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<210> 56
 <211> 282
 <212> PRT
 <213> Mus musculus

<220>
 <223> mouse protein-kinase C-related kinase 1 (PRK1),
 protein-kinase C-like 1, serine/threonine protein
 kinase N (PKN)

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 20 25 30
 Phe Val Met Glu Tyr Ser Ala Gly Gly Asp Leu Met Leu His Ile His
 35 40 45
 Ser Asp Val Phe Ser Glu Pro Arg Ala Val Phe Tyr Ser Ala Cys Val
 50 55 60
 Val Leu Gly Leu Gln Phe Leu His Glu His Lys Ile Val Tyr Arg Asp
 65 70 75 80
 Leu Lys Leu Asp Asn Leu Leu Leu Asp Thr Glu Gly Tyr Val Lys Ile
 85 90 95
 Ala Asp Phe Gly Leu Cys Lys Glu Gly Met Gly Tyr Gly Asp Arg Thr
 100 105 110
 Ser Thr Phe Cys Gly Thr Pro Glu Phe Leu Ala Pro Glu Val Leu Thr
 115 120 125
 Asp Thr Ser Tyr Thr Arg Ala Val Asp Trp Trp Gly Leu Gly Val Leu
 130 135 140
 Leu Tyr Glu Met Leu Val Gly Glu Ser Pro Phe Pro Gly Asp Asp Glu
 145 150 155 160

Glu Glu Val Phe Asp Ser Ile Val Asn Asp Glu Val Arg Tyr Pro Arg
 165 170 175
 Phe Leu Ser Ala Glu Ala Ile Gly Ile Met Arg Arg Leu Leu Arg Arg
 180 185 190
 Asn Pro Glu Arg Arg Leu Gly Ser Thr Glu Arg Asp Ala Glu Asp Val
 195 200 205
 Lys Lys Gln Pro Phe Phe Arg Ser Leu Gly Trp Asp Val Leu Leu Ala
 210 215 220
 Arg Arg Leu Pro Pro Pro Phe Val Pro Thr Leu Ser Gly Arg Thr Asp
 225 230 235 240
 Val Ser Asn Phe Asp Glu Glu Phe Thr Gly Glu Ala Pro Thr Leu Ser
 245 250 255
 Pro Pro Arg Asp Ala Arg Pro Leu Thr Ala Ala Glu Gln Ala Ala Phe
 260 265 270
 Arg Asp Phe Asp Phe Val Ala Gly Gly Tyr
 275 280

<210> 57
 <211> 2936
 <212> DNA
 <213> Rattus norvegicus

<220>
 <223> rat protein-kinase C-related kinase 1 (PRK1),
 cardiolipin/protease-activated protein kinase -1
 (PAK-1) cDNA

<220>
 <221> CDS
 <222> (18)..(2858)
 <223> PRK1

<400> 57
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 gcagacccaa ggaccggaag ctgctgttga cggcccaaca gatgctgcag gatagtaaga 540
 ccaagattga catcatccgc atgcagcttc gccgggcgct acaagcactc caggctggcc 600
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<210> 58
<211> 946
<212> PRT
<213> Rattus norvegicus

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<220>
<223> rat protein-kinase C-related kinase 1 (PRK1),
      cardiolipin/protease-activated protein kinase -1
      (PAK-1)

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<400> 58
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Glu Gln Leu Gly Leu Ala Gly Ala Asp Leu Ala Ala Pro Gly Val Gln
      20             25             30

Gln Gln Leu Glu Leu Glu Arg Glu Arg Leu Lys Arg Glu Ile Arg Lys
      35             40             45

Glu Leu Lys Leu Lys Glu Gly Ala Glu Asn Leu Arg Arg Ala Thr Thr
      50             55             60

Asp Leu Gly Arg Ser Leu Ala Pro Val Glu Leu Leu Arg Gly Ser
      65             70             75             80

Ala Arg Arg Leu Asp Leu Leu His Gln Gln Leu Gln Glu Leu His Ala
      85             90             95

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His	Val	Val	Leu	Pro	Asp	Pro	Thr	Ala	Gly	Ser	Asp	Ala	Pro	Gln	Ser		
			100					105					110				
Leu	Ala	Glu	Gly	Ser	Pro	Val	Cys	Ser	Ser	Thr	Asn	Leu	Ser	Arg	Val		
		115					120					125					
Ala	Gly	Leu	Glu	Lys	Gln	Leu	Ala	Ile	Glu	Leu	Lys	Val	Lys	Gln	Gly		
	130					135					140						
Ala	Glu	Asn	Met	Ile	Gln	Thr	Tyr	Ser	Asn	Gly	Ser	Thr	Lys	Asp	Arg		
145					150					155					160		
Lys	Leu	Leu	Leu	Thr	Ala	Gln	Gln	Met	Leu	Gln	Asp	Ser	Lys	Thr	Lys		
				165					170					175			
Ile	Asp	Ile	Ile	Arg	Met	Gln	Leu	Arg	Arg	Ala	Leu	Gln	Ala	Leu	Gln		
		180						185					190				
Ala	Gly	Gln	Leu	Glu	Ser	Gln	Ala	Ala	Pro	Asp	Glu	Ala	His	Gly	Asp		
		195					200					205					
Pro	Asp	Leu	Gly	Ala	Val	Glu	Leu	Arg	Ile	Glu	Glu	Leu	Arg	His	His		
	210					215					220						
Phe	Arg	Val	Glu	His	Ala	Val	Ala	Glu	Gly	Ala	Lys	Asn	Val	Leu	Arg		
225					230					235					240		
Leu	Leu	Ser	Ala	Ala	Lys	Ala	Pro	Asp	Arg	Lys	Ala	Val	Ser	Glu	Ala		
			245						250					255			
Gln	Glu	Lys	Leu	Thr	Glu	Ser	Asn	Gln	Lys	Leu	Gly	Leu	Leu	Arg	Glu		
		260						265						270			
Ser	Leu	Glu	Arg	Arg	Leu	Gly	Glu	Leu	Pro	Ala	Asp	His	Pro	Lys	Gly		
		275					280					285					
Arg	Leu	Leu	Arg	Glu	Glu	Leu	Thr	Ala	Arg	Ser	Ser	Ala	Ala	Phe	Ser		
	290					295					300						
Ala	Ile	Leu	Pro	Gly	Pro	Phe	Pro	Ala	Thr	His	Tyr	Ser	Thr	Leu	Ser		
305					310					315					320		
Lys	Pro	Ala	Pro	Leu	Thr	Gly	Thr	Leu	Glu	Val	Arg	Val	Val	Gly	Cys		
			325						330					335			
Lys	Asn	Leu	Pro	Glu	Thr	Ile	Pro	Trp	Ser	Pro	Pro	Pro	Ser	Val	Gly		
		340						345					350				
Ala	Ser	Gly	Thr	Pro	Asp	Ser	Arg	Thr	Pro	Phe	Leu	Ser	Arg	Pro	Ala		
		355					360					365					
Arg	Gly	Leu	Tyr	Asn	Arg	Ser	Gly	Ser	Leu	Ser	Gly	Arg	Ser	Ser	Leu		
	370					375					380						
Lys	Gly	Glu	Ala	Glu	Asn	Ser	Thr	Glu	Val	Ser	Thr	Val	Leu	Lys	Leu		
385					390					395					400		
Asp	Asn	Thr	Val	Val	Gly	Gln	Thr	Ala	Trp	Lys	Pro	Cys	Gly	Pro	Asn		
			405						410					415			

Ala	Trp	Asp	Gln	Ser	Phe	Thr	Leu	Glu	Leu	Glu	Arg	Ala	Arg	Glu	Leu	420	425	430	
Glu	Leu	Ala	Val	Phe	Trp	Arg	Asp	Gln	Arg	Gly	Leu	Cys	Ala	Leu	Lys	435	440	445	
Phe	Leu	Lys	Leu	Glu	Asp	Phe	Leu	Asp	Asn	Glu	Arg	His	Glu	Val	Gln	450	455	460	
Leu	Asp	Met	Glu	Pro	Gln	Gly	Cys	Leu	Val	Ala	Glu	Val	Thr	Phe	Arg	465	470	475	480
Asn	Pro	Ile	Ile	Glu	Arg	Ile	Pro	Arg	Leu	Gln	Arg	Gln	Lys	Lys	Ile	485	490	495	
Phe	Ser	Lys	Gln	Gln	Gly	Gln	Thr	Phe	Gln	Arg	Ala	Arg	Gln	Met	Asn	500	505	510	
Ile	Asp	Val	Ala	Thr	Trp	Val	Arg	Leu	Leu	Arg	Arg	Leu	Ile	Pro	Asn	515	520	525	
Ala	Val	Ala	Thr	Gly	Ser	Phe	Ser	Pro	Asn	Ala	Ser	Pro	Gly	Ser	Glu	530	535	540	
Ile	Arg	Ser	Thr	Gly	Asp	Ile	Ser	Met	Glu	Lys	Leu	Asn	Leu	Gly	Ala	545	550	555	560
Asp	Ser	Asp	Ser	Ser	Ser	Gln	Lys	Ser	Pro	Ala	Gly	Leu	Pro	Ser	Thr	565	570	575	
Ser	Cys	Ser	Leu	Ser	Ser	Pro	Thr	His	Glu	Ser	Thr	Thr	Ser	Pro	Glu	580	585	590	
Leu	Pro	Ser	Glu	Thr	Gln	Glu	Thr	Pro	Gly	Pro	Gly	Leu	Cys	Ser	Pro	595	600	605	
Leu	Arg	Lys	Ser	Pro	Leu	Thr	Leu	Glu	Asp	Phe	Lys	Phe	Leu	Ala	Val	610	615	620	
Leu	Gly	Arg	Gly	His	Phe	Gly	Lys	Val	Leu	Leu	Ser	Glu	Phe	His	Ser	625	630	635	640
Ser	Gly	Glu	Leu	Phe	Ala	Ile	Lys	Ala	Val	Lys	Lys	Gly	Asp	Ile	Val	645	650	655	
Ala	Arg	Asp	Glu	Val	Glu	Ser	Leu	Met	Cys	Glu	Lys	Arg	Ile	Leu	Ala	660	665	670	
Thr	Val	Thr	Arg	Ala	Gly	His	Pro	Phe	Leu	Val	Asn	Leu	Phe	Gly	Cys	675	680	685	
Phe	Gln	Thr	Pro	Glu	His	Val	Cys	Phe	Val	Met	Glu	Tyr	Ser	Ala	Gly	690	695	700	
Gly	Asp	Leu	Met	Leu	His	Ile	His	Ser	Asp	Val	Phe	Ser	Glu	Pro	Arg	705	710	715	720
Ala	Val	Phe	Tyr	Ser	Ala	Cys	Val	Val	Leu	Gly	Leu	Gln	Phe	Leu	His	725	730	735	

Glu His Lys Ile Val Tyr Arg Asp Leu Lys Leu Asp Asn Leu Leu Leu
 740 745 750
 Asp Thr Glu Gly Tyr Val Lys Ile Ala Asp Phe Gly Leu Cys Lys Glu
 755 760 765
 Gly Met Gly Tyr Gly Asp Arg Thr Ser Thr Phe Cys Gly Thr Pro Glu
 770 775 780
 Phe Leu Ala Pro Glu Val Leu Thr Asp Thr Ser Tyr Thr Arg Ala Val
 785 790 795 800
 Asp Trp Trp Gly Leu Gly Val Leu Leu Tyr Glu Met Leu Val Gly Glu
 805 810 815
 Ser Pro Phe Pro Gly Asp Asp Glu Glu Glu Val Phe Asp Ser Ile Val
 820 825 830
 Asn Asp Glu Val Arg Tyr Pro Arg Phe Leu Ser Ala Glu Ala Ile Gly
 835 840 845
 Ile Met Arg Arg Leu Leu Arg Arg Asn Pro Glu Arg Arg Leu Gly Ser
 850 855 860
 Thr Glu Arg Asp Ala Glu Asp Val Lys Lys Gln Pro Phe Phe Arg Thr
 865 870 875 880
 Leu Asp Trp Asp Ala Leu Leu Ala Arg Arg Leu Pro Pro Pro Phe Val
 885 890 895
 Pro Thr Leu Ser Gly Arg Thr Asp Val Ser Asn Phe Asp Glu Glu Phe
 900 905 910
 Thr Gly Glu Ala Pro Thr Leu Ser Pro Pro Arg Asp Ala Arg Pro Leu
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 Thr Ala Ala Glu Gln Ala Ala Phe Arg Asp Phe Asp Phe Val Ala Gly
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 Gly Tyr
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<210> 59
 <211> 1292
 <212> DNA
 <213> Homo sapiens

<220>
 <223> human hydroxyindole-O-methyltransferase (HIOMT)
 cDNA

<220> \
 <221> CDS
 <222> (104)..(1225)
 <223> HIOMT

<400> 59
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 ccaggcctat cgcctcctta atgactacgc caacggcttc atggtgtccc aggttctctt 180

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cgccgcctgc gagctgggcg tgtttgacct tctcgccgag gccccagggc ccttggacgt 240
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cacagagctg tccagcgact acctgaccac ggtcagcccg acgtcacaat gcagcatgct 420
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<210> 60
<211> 373
<212> PRT
<213> Homo sapiens

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<220>
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Asn Gly Phe Met Val Ser Gln Val Leu Phe Ala Ala Cys Glu Leu Gly
          20                      25          30

Val Phe Asp Leu Leu Ala Glu Ala Pro Gly Pro Leu Asp Val Ala Ala
          35                      40          45

Val Ala Ala Gly Val Arg Ala Ser Ala His Gly Thr Glu Leu Leu Leu
          50                      55          60

Asp Ile Cys Val Ser Leu Lys Leu Leu Lys Val Glu Thr Arg Gly Gly
          65                      70          75          80

Lys Ala Phe Tyr Arg Asn Thr Glu Leu Ser Ser Asp Tyr Leu Thr Thr
          85                      90          95

Val Ser Pro Thr Ser Gln Cys Ser Met Leu Lys Tyr Met Gly Arg Thr
          100                     105          110

Ser Tyr Arg Cys Trp Gly His Leu Ala Asp Ala Val Arg Glu Gly Arg
          115                     120          125

Asn Gln Tyr Leu Glu Thr Phe Gly Val Pro Ala Glu Glu Leu Phe Thr
          130                     135          140

Ala Ile Tyr Arg Ser Glu Gly Glu Arg Leu Gln Phe Met Gln Ala Leu
          145                     150          155          160

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Gln Glu Val Trp Ser Val Asn Gly Arg Ser Val Leu Thr Ala Phe Asp
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 195 200 205
 His Arg Val Phe Ser Leu Ile Gly Gly Ala Gly Ala Leu Ala Lys Glu
 210 215 220
 Cys Met Ser Leu Tyr Pro Gly Cys Lys Ile Thr Val Phe Asp Ile Pro
 225 230 235 240
 Glu Val Val Trp Thr Ala Lys Gln His Phe Ser Phe Gln Glu Glu Glu
 245 250 255
 Gln Ile Asp Phe Gln Glu Gly Asp Phe Phe Lys Asp Pro Leu Pro Glu
 260 265 270
 Ala Asp Leu Tyr Ile Leu Ala Arg Val Leu His Asp Trp Ala Asp Gly
 275 280 285
 Lys Cys Ser His Leu Leu Glu Arg Ile Tyr His Thr Cys Lys Pro Gly
 290 295 300
 Gly Gly Ile Leu Val Ile Glu Ser Leu Leu Asp Glu Asp Arg Arg Gly
 305 310 315 320
 Pro Leu Leu Thr Gln Leu Tyr Ser Leu Asn Met Leu Val Gln Thr Glu
 325 330 335
 Gly Gln Glu Arg Thr Pro Thr His Tyr His Met Leu Leu Ser Ser Ala
 340 345 350
 Gly Phe Arg Asp Phe Gln Phe Lys Lys Thr Gly Ala Ile Tyr Asp Ala
 355 360 365
 Ile Leu Ala Arg Lys
 370

<210> 61

<211> 3969

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Asp Phe Val Leu Ser Val Ala Gly Gly Phe Val Gly Leu Gly Asn Val
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Trp Arg Phe Pro Tyr Leu Cys Tyr Lys Asn Gly Gly Gly Ala Phe Leu
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Ile Pro Tyr Phe Ile Phe Leu Phe Gly Ser Gly Leu Pro Val Phe Phe
85 90 95
Leu Glu Ile Ile Ile Gly Gln Tyr Thr Ser Glu Gly Gly Ile Thr Cys
100 105 110
Trp Glu Lys Ile Cys Pro Leu Phe Ser Gly Ile Gly Tyr Ala Ser Val
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His Cys Asn His Ser Trp Asn Thr Pro His Cys Met Glu Asp Thr Met
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Arg Lys Asn Lys Ser Val Trp Ile Thr Ile Ser Ser Thr Asn Phe Thr
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195 200 205
Gly Ile Asp His Pro Gly Ser Leu Lys Trp Asp Leu Ala Leu Cys Leu
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Ser Thr Gly Lys Val Val Tyr Phe Thr Ala Thr Phe Pro Phe Ala Met
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 Gly Ile Lys Phe Tyr Leu Tyr Pro Asp Ile Thr Arg Leu Glu Asp Pro
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 Gln Val Trp Ile Asp Ala Gly Thr Gln Ile Phe Phe Ser Tyr Ala Ile
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 Cys Leu Gly Ala Met Thr Ser Leu Gly Ser Tyr Asn Lys Tyr Lys Tyr
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 Gly Tyr Arg Pro Gly Pro Trp Met Lys Tyr Ser Trp Val Ile Thr Pro
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<212> PRT
<213> Mus musculus

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Asp Phe Val Leu Ser Val Ala Gly Gly Phe Val Gly Leu Gly Asn Val
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Trp Arg Phe Pro Tyr Leu Cys Tyr Lys Asn Gly Gly Gly Ala Phe Leu
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Ile Pro Tyr Phe Ile Phe Leu Phe Gly Ser Gly Leu Pro Val Phe Phe
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Leu Glu Val Ile Ile Gly Gln Tyr Thr Ser Glu Gly Gly Ile Thr Cys
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Trp Glu Lys Ile Cys Pro Leu Phe Ser Gly Ile Gly Tyr Ala Ser Ile
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Val Ile Val Ser Leu Leu Asn Val Tyr Tyr Ile Val Ile Leu Ala Trp
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Ala Thr Tyr Tyr Leu Phe His Ser Phe Gln Lys Asp Leu Pro Trp Ala
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His Cys Asn His Ser Trp Asn Thr Pro Gln Cys Met Glu Asp Thr Leu
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Arg Arg Asn Glu Ser His Trp Val Ser Leu Ser Thr Ala Asn Phe Thr
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Ser Pro Val Ile Glu Phe Trp Glu Arg Asn Val Leu Ser Leu Ser Ser
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Gly Ile Asp Asn Pro Gly Ser Leu Lys Trp Asp Leu Ala Leu Cys Leu
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 member 6 cDNA

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 tgtttcatct tctctctcgt caagtatgta cccctgacct acaacaaagt ctaccggtac 1740
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tgtgtttcgt gtgtgtctgt atatgtgtat tttgttttat ttgggggatt attttgtaca 2220
aaaagaaaaa ccatgggcct atgtcctggg gggagaggat ggactttcat attgattttg 2280
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tgcccaaaaa caaatgaaaa aaaaaaaaaa 2489

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<210> 66
<211> 621
<212> PRT
<213> Rattus norvegicus

```

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<220>
<223> rat taurine transporter, solute carrier family 6,
      member 6

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<400> 66
Met Ala Thr Lys Glu Lys Leu Gln Cys Leu Lys Asp Phe His Lys Asp
  1             5             10             15

Ile Leu Lys Pro Ser Pro Gly Lys Ser Pro Gly Thr Arg Pro Glu Asp
             20             25             30

Glu Ala Asp Gly Lys Pro Pro Gln Arg Glu Lys Trp Ser Ser Lys Ile
  35             40             45

Asp Phe Val Leu Ser Val Ala Gly Gly Phe Val Gly Leu Gly Asn Val
  50             55             60

Trp Arg Phe Pro Tyr Leu Cys Tyr Lys Asn Gly Gly Gly Ala Phe Leu
  65             70             75             80

Ile Pro Tyr Phe Ile Phe Leu Phe Gly Ser Gly Leu Pro Val Phe Phe
             85             90             95

Leu Glu Val Ile Ile Gly Gln Tyr Thr Ser Glu Gly Gly Ile Thr Cys
  100            105            110

Trp Glu Lys Ile Cys Pro Leu Phe Ser Gly Ile Gly Tyr Ala Ser Ile
  115            120            125

Val Ile Val Ser Leu Leu Asn Val Tyr Tyr Ile Val Ile Leu Ala Trp
  130            135            140

Ala Thr Tyr Tyr Leu Phe Gln Ser Phe Gln Lys Asp Leu Pro Trp Ala
  145            150            155            160

His Cys Asn His Ser Trp Asn Thr Pro Gln Cys Met Glu Asp Thr Leu
             165            170            175

Arg Arg Asn Glu Ser His Trp Val Ser Leu Ser Ala Ala Asn Phe Thr
  180            185            190

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Ser Pro Val Ile Glu Phe Trp Glu Arg Asn Val Leu Ser Leu Ser Ser
 195 200 205
 Gly Ile Asp His Pro Gly Ser Leu Lys Trp Asp Leu Ala Leu Cys Leu
 210 215 220
 Leu Leu Val Trp Leu Val Cys Phe Phe Cys Ile Trp Lys Gly Val Arg
 225 230 235 240
 Ser Thr Gly Lys Val Val Tyr Phe Thr Ala Thr Phe Pro Phe Ala Met
 245 250 255
 Leu Leu Val Leu Leu Val Arg Gly Leu Thr Leu Pro Gly Ala Gly Glu
 260 265 270
 Gly Ile Lys Phe Tyr Leu Tyr Pro Asn Ile Ser Arg Leu Glu Asp Pro
 275 280 285
 Gln Val Trp Ile Asp Ala Gly Thr Gln Ile Phe Phe Ser Tyr Ala Ile
 290 295 300
 Cys Leu Gly Ala Met Thr Ser Leu Gly Ser Tyr Asn Lys Tyr Lys Tyr
 305 310 315 320
 Asn Ser Tyr Arg Asp Cys Met Leu Leu Gly Cys Leu Asn Ser Gly Thr
 325 330 335
 Ser Phe Val Ser Gly Phe Ala Ile Phe Ser Ile Leu Gly Phe Met Ala
 340 345 350
 Gln Glu Gln Gly Val Asp Ile Ala Asp Val Ala Glu Ser Gly Pro Gly
 355 360 365
 Leu Ala Phe Ile Ala Tyr Pro Lys Ala Val Thr Met Met Pro Leu Pro
 370 375 380
 Thr Phe Trp Ser Ile Leu Phe Phe Ile Met Leu Leu Leu Leu Gly Leu
 385 390 395 400
 Asp Ser Gln Phe Val Glu Val Glu Gly Gln Ile Thr Ser Leu Val Asp
 405 410 415
 Leu Tyr Pro Ser Phe Leu Arg Lys Gly Tyr Arg Arg Glu Ile Phe Ile
 420 425 430
 Ala Ile Val Cys Ser Ile Ser Tyr Leu Leu Gly Leu Thr Met Val Thr
 435 440 445
 Glu Gly Gly Met Tyr Val Phe Gln Leu Phe Asp Tyr Tyr Ala Ala Ser
 450 455 460
 Gly Val Cys Leu Leu Trp Val Ala Phe Phe Glu Cys Phe Val Ile Ala
 465 470 475 480
 Trp Ile Tyr Gly Gly Asp Asn Leu Tyr Asp Gly Ile Glu Asp Met Ile
 485 490 495
 Gly Tyr Arg Pro Gly Pro Trp Met Lys Tyr Ser Trp Ala Val Ile Thr
 500 505 510

Pro Ala Leu Cys Val Gly Cys Phe Ile Phe Ser Leu Val Lys Tyr Val
 515 520 525
 Pro Leu Thr Tyr Asn Lys Val Tyr Arg Tyr Pro Asp Trp Ala Ile Gly
 530 535 540
 Leu Gly Trp Gly Leu Ala Leu Ser Ser Met Val Cys Ile Pro Leu Val
 545 550 555 560
 Ile Val Ile Leu Leu Cys Arg Thr Glu Gly Pro Leu Arg Val Arg Ile
 565 570 575
 Lys Tyr Leu Ile Thr Pro Arg Glu Pro Asn Arg Trp Ala Val Glu Arg
 580 585 590
 Glu Gly Ala Thr Pro Phe His Ser Arg Ala Thr Leu Met Asn Gly Ala
 595 600 605
 Leu Met Lys Pro Ser His Val Ile Val Glu Thr Met Met
 610 615 620

<210> 67
 <211> 1594
 <212> DNA
 <213> Homo sapiens

<220>
 <223> human (R)-3-hydroxybutyrate dehydrogenase (BDH)
 cDNA

<220>
 <221> CDS
 <222> (224)..(1255)
 <223> BDH

<400> 67
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 gtgaaggcga gagcctcggc gagccctctg cagcggagcc ccctgcccac ttgggttttg 180
 aaccaccgga aggaactggg ccatttctaac acccgttgct accatgctgg ccaccgcct 240
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 ttttaacact aactagaggg aatgacttct ttgcatagtg agtgacttgg gccttcacaa 1440

acagggtgtg gagtggcagg cagaggcctc taaatctcag ggcaaacatg gtgaatctat 1500
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<210> 68
 <211> 343
 <212> PRT
 <213> Homo sapiens

<220>
 <223> human (R)-3-hydroxybutyrate dehydrogenase (BDH)

<400> 68
 Met Leu Ala Thr Arg Leu Ser Arg Pro Leu Ser Arg Leu Pro Gly Lys
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 Thr Leu Ser Ala Cys Asp Arg Glu Asn Gly Ala Arg Arg Pro Leu Leu
 20 25 30
 Leu Gly Ser Thr Ser Phe Ile Pro Ile Gly Arg Arg Thr Tyr Ala Ser
 35 40 45
 Ala Ala Glu Pro Val Gly Ser Lys Ala Val Leu Val Thr Gly Cys Asp
 50 55 60
 Ser Gly Phe Gly Phe Ser Leu Ala Lys His Leu His Ser Lys Gly Phe
 65 70 75 80
 Leu Val Phe Ala Gly Cys Leu Met Lys Asp Lys Gly His Asp Gly Val
 85 90 95
 Lys Glu Leu Asp Ser Leu Asn Ser Asp Arg Leu Arg Thr Val Gln Leu
 100 105 110
 Asn Val Cys Ser Ser Glu Glu Val Glu Lys Val Val Glu Ile Val Arg
 115 120 125
 Ser Ser Leu Lys Asp Pro Glu Lys Gly Met Trp Gly Leu Val Asn Asn
 130 135 140
 Ala Gly Ile Ser Thr Phe Gly Glu Val Glu Phe Thr Ser Leu Glu Thr
 145 150 155 160
 Tyr Lys Gln Val Ala Glu Val Asn Leu Trp Gly Thr Val Arg Met Thr
 165 170 175
 Lys Ser Phe Leu Pro Leu Ile Arg Arg Ala Lys Gly Arg Val Val Asn
 180 185 190
 Ile Ser Ser Met Leu Gly Arg Met Ala Asn Pro Ala Arg Ser Pro Tyr
 195 200 205
 Cys Ile Thr Lys Phe Gly Val Glu Ala Phe Ser Asp Cys Leu Arg Tyr
 210 215 220
 Glu Met Tyr Pro Leu Gly Val Lys Val Ser Val Val Glu Pro Gly Asn
 225 230 235 240
 Phe Ile Ala Ala Thr Ser Leu Tyr Ser Pro Glu Ser Ile Gln Ala Ile
 245 250 255

Ala Lys Lys Met Trp Glu Glu Leu Pro Glu Val Val Arg Lys Asp Tyr
260 265 270

Gly Lys Lys Tyr Phe Asp Glu Lys Ile Ala Lys Met Glu Thr Tyr Cys
275 280 285

Ser Ser Gly Ser Thr Asp Thr Ser Pro Val Ile Asp Ala Val Thr His
290 295 300

Ala Leu Thr Ala Thr Thr Pro Tyr Thr Arg Tyr His Pro Met Asp Tyr
305 310 315 320

Tyr Trp Trp Leu Arg Met Gln Ile Met Thr His Leu Pro Gly Ala Ile
325 330 335

Ser Asp Met Ile Tyr Ile Arg
340

<210> 69
<211> 2592
<212> DNA
<213> Mus musculus

<220>
<223> mouse (R)-3-hydroxybutyrate dehydrogenase (BDH)
partial cDNA

<220>
<221> CDS
<222> (2)..(766)
<223> BDH

<400> 69
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gtttggggag gtggagttca ccagcatgga gacatataag gaggtggctg aagtgaacct 240
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aaaaaaaaaa aa 2592

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<210> 70

<211> 254

<212> PRT

<213> Mus musculus

<220>

<223> mouse (R)-3-hydroxybutyrate dehydrogenase (BDH),
partial

<400> 70

Asp Lys Gly Asp Ala Gly Val Lys Glu Leu Asp Ser Leu Lys Ser Asp
1 5 10 15

Arg Leu Arg Thr Ile Gln Leu Asn Val Cys Asn Ser Glu Glu Val Glu
20 25 30

Lys Ala Val Glu Thr Ile Arg Ser Gly Leu Lys Asp Pro Glu Lys Gly
35 40 45

Met Trp Gly Leu Val Asn Asn Ala Gly Ile Ser Thr Phe Gly Glu Val
50 55 60

Glu Phe Thr Ser Met Glu Thr Tyr Lys Glu Val Ala Glu Val Asn Leu
65 70 75 80

Trp Gly Thr Val Arg Thr Thr Lys Ser Phe Leu Pro Leu Leu Arg Arg
85 90 95

Ala Lys Gly Arg Val Val Asn Ile Ser Ser Met Leu Gly Arg Met Ala
100 105 110

Asn Pro Ala Arg Ser Pro Tyr Cys Ile Thr Lys Phe Gly Val Glu Ala
115 120 125

Phe Ser Asp Cys Leu Arg Tyr Glu Met His Pro Leu Gly Val Lys Val
130 135 140

Ser Val Val Glu Pro Gly Asn Phe Ile Ala Ala Thr Ser Leu Tyr Ser
145 150 155 160

Pro Glu Arg Ile Gln Ala Ile Ala Lys Lys Met Trp Asp Asp Leu Pro
165 170 175

Glu Val Val Arg Lys Asp Tyr Gly Arg Lys Tyr Phe Asp Glu Lys Ile
 180 185 190
 Ala Lys Met Glu Thr Tyr Cys Asn Ser Gly Ser Thr Asp Thr Ser Ser
 195 200 205
 Val Ile Asn Ala Val Thr His Ala Leu Thr Ala Ala Thr Pro Tyr Thr
 210 215 220
 Arg Tyr His Pro Met Asp Tyr Tyr Trp Trp Leu Arg Met Gln Ile Met
 225 230 235 240
 Thr His Phe Pro Gly Ala Ile Ser Asp Lys Ile Tyr Ile His
 245 250

<210> 71
 <211> 1420
 <212> DNA
 <213> Rattus norvegicus

<220>
 <223> rat (R)-3-hydroxybutyrate dehydrogenase (BDH) cDNA

<220>
 <221> CDS
 <222> (96)..(1130)
 <223> BDH

<400> 71
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 gacctctgtc acagctccca ggaaaagctc taagtgtctg tgatagagaa aatgggacaa 180
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 gccaggcaga tgcggctagt ggcaaagctg tcctgggttac aggctgtgac tctggatttg 300
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 caacgttttg ggaggtggag ttcactagca tggagacgta taaggaggtg gccgaagtga 600
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 gccgtgttgt taacatcagc agcatgctgg gtcgcatggc caaccagacc cgctcaccat 720
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 aaataccttt atattaaaga cgttattaga atagaaaaaa 1420

<210> 72
 <211> 344
 <212> PRT
 <213> Rattus norvegicus

<220>

<223> rat (R)-3-hydroxybutyrate dehydrogenase (BDH)

<400> 72

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Met Met Leu Ala Ala Arg Leu Ser Arg Pro Leu Ser Gln Leu Pro Gly
  1              5              10              15

Lys Ala Leu Ser Val Cys Asp Arg Glu Asn Gly Thr Arg His Thr Leu
      20              25              30

Leu Phe Tyr Pro Ala Ser Phe Ser Pro Asp Thr Arg Arg Thr Tyr Thr
      35              40              45

Ser Gln Ala Asp Ala Ala Ser Gly Lys Ala Val Leu Val Thr Gly Cys
      50              55              60

Asp Ser Gly Phe Gly Phe Ser Leu Ala Lys His Leu His Ser Lys Gly
      65              70              75              80

Phe Leu Val Phe Ala Gly Cys Leu Leu Lys Glu Gln Gly Asp Ala Gly
      85              90              95

Val Arg Glu Leu Asp Ser Leu Lys Ser Asp Arg Leu Arg Thr Ile Gln
      100             105             110

Leu Asn Val Cys Asn Ser Glu Glu Val Glu Lys Ala Val Glu Thr Val
      115             120             125

Arg Ser Gly Leu Lys Asp Pro Glu Lys Gly Met Trp Gly Leu Val Asn
      130             135             140

Asn Ala Gly Ile Ser Thr Phe Gly Glu Val Glu Phe Thr Ser Met Glu
      145             150             155             160

Thr Tyr Lys Glu Val Ala Glu Val Asn Leu Trp Gly Thr Val Arg Thr
      165             170             175

Thr Lys Ser Phe Leu Pro Leu Leu Arg Arg Ala Lys Gly Arg Val Val
      180             185             190

Asn Ile Ser Ser Met Leu Gly Arg Met Ala Asn Pro Ala Arg Ser Pro
      195             200             205

Tyr Cys Ile Thr Lys Phe Gly Val Glu Ala Phe Ser Asp Cys Leu Arg
      210             215             220

Tyr Glu Met His Pro Leu Gly Val Lys Val Ser Val Val Glu Pro Gly
      225             230             235             240

Asn Phe Ile Ala Ala Thr Ser Leu Tyr Ser Pro Glu Arg Ile Gln Ala
      245             250             255

Ile Ala Lys Lys Met Trp Asp Glu Leu Pro Glu Val Val Arg Lys Asp
      260             265             270

Tyr Gly Lys Lys Tyr Phe Asp Glu Lys Ile Ala Lys Met Glu Thr Tyr
      275             280             285

Cys Asn Ser Gly Ser Thr Asp Thr Ser Ser Val Ile Asn Ala Val Thr
      290             295             300
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His Ala Leu Thr Ala Ala Thr Pro Tyr Thr Arg Tyr His Pro Met Asp
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Tyr Tyr Trp Trp Leu Arg Met Gln Val Met Thr His Phe Pro Gly Ala
 325 330 335

Ile Ser Asp Lys Ile Tyr Ile His
 340

<210> 73
 <211> 1132
 <212> DNA
 <213> Homo sapiens

<220>
 <223> human aldehyde reductase (ALDR1) cDNA

<220>
 <221> CDS
 <222> (61)..(1038)
 <223> aldehyde reductase

<400> 73
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 gctgtcttgc aggtggaatg ccacccatac ttggctcaaa atgagctaag tgcccactgc 660
 caagcacgtg gcttggagggt aactgcttat agccctttgg gctcctctga tcgtgcatgg 720
 cgtgatcctg atgagcctgt cctgctggag gaaccagtag tcctggcatt ggctgaaaag 780
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 aggtcctgcc acaacggaaa gagggagtta ataaagccat tggagcatcc at 1132

<210> 74
 <211> 325
 <212> PRT
 <213> Homo sapiens

<220>
 <223> human aldehyde reductase (ALDR1)

<400> 74
 Met Ala Ala Ser Cys Val Leu Leu His Thr Gly Gln Lys Met Pro Leu
 1 5 10 15

Ile Gly Leu Gly Thr Trp Lys Ser Glu Pro Gly Gln Val Lys Ala Ala
 20 25 30

Val Lys Tyr Ala Leu Ser Val Gly Tyr Arg His Ile Asp Cys Ala Ala
35 40 45
Ile Tyr Gly Asn Glu Pro Glu Ile Gly Glu Ala Leu Lys Glu Asp Val
50 55 60
Gly Pro Gly Lys Ala Val Pro Arg Glu Glu Leu Phe Val Thr Ser Lys
65 70 75 80
Leu Trp Asn Thr Lys His His Pro Glu Asp Val Glu Pro Ala Leu Arg
85 90 95
Lys Thr Leu Ala Asp Leu Gln Leu Glu Tyr Leu Asp Leu Tyr Leu Met
100 105 110
His Trp Pro Tyr Ala Phe Glu Arg Gly Asp Asn Pro Phe Pro Lys Asn
115 120 125
Ala Asp Gly Thr Ile Cys Tyr Asp Ser Thr His Tyr Lys Glu Thr Trp
130 135 140
Lys Ala Leu Glu Ala Leu Val Ala Lys Gly Leu Val Gln Ala Leu Gly
145 150 155 160
Leu Ser Asn Phe Asn Ser Arg Gln Ile Asp Asp Ile Leu Ser Val Ala
165 170 175
Ser Val Arg Pro Ala Val Leu Gln Val Glu Cys His Pro Tyr Leu Ala
180 185 190
Gln Asn Glu Leu Ile Ala His Cys Gln Ala Arg Gly Leu Glu Val Thr
195 200 205
Ala Tyr Ser Pro Leu Gly Ser Ser Asp Arg Ala Trp Arg Asp Pro Asp
210 215 220
Glu Pro Val Leu Leu Glu Glu Pro Val Val Leu Ala Leu Ala Glu Lys
225 230 235 240
Tyr Gly Arg Ser Pro Ala Gln Ile Leu Leu Arg Trp Gln Val Gln Arg
245 250 255
Lys Val Ile Cys Ile Pro Lys Ser Ile Thr Pro Ser Arg Ile Leu Gln
260 265 270
Asn Ile Lys Val Phe Asp Phe Thr Phe Ser Pro Glu Glu Met Lys Gln
275 280 285
Leu Asn Ala Leu Asn Lys Asn Trp Arg Tyr Ile Val Pro Met Leu Thr
290 295 300
Val Asp Gly Lys Arg Val Pro Arg Asp Ala Gly His Pro Leu Tyr Pro
305 310 315 320
Phe Asn Asp Pro Tyr
325

<210> 75
 <211> 1320
 <212> DNA
 <213> Mus musculus

<220>
 <223> mouse aldo-keto reductase family 1, member A4
 (aldehyde reductase) (Akrla4) cDNA

<220>
 <221> CDS
 <222> (248)..(1225)
 <223> aldehyde reductase

<400> 75
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 aggacagtgg ggggtctcctc cgtcctgcgc gtagttctgg gagccgggccc ctcgctcctc 120
 cctgggggtgg ggctgccgct tctccgcccg gacttaagtc gggccctgtt gcctcagtac 180
 tggagtgcag agctgaattc gggccacttt gtcttttcca cagcctgtgc tcaactgcaa 240
 ggggacaatg acggcctcca gtgtcctcct gcacactgga cagaagatgc ctctgattgg 300
 tctgggggaca tggaagagtg agcctgggtca ggtgaaagca gccattaaac atgcccttag 360
 cgcaggctac cgccacattg attgtgcttc tgtatatggc aatgaaactg agattgggga 420
 ggccctgaag gagagtgtgg ggtcaggcaa ggcagtcctc cgagaggagc tgtttgtgac 480
 atccaagctg tggaataacta agcaccaccc tgaggatgta gaacctgccc tccggaagac 540
 actggctgat ctgcaactgg agtattttgga cctctatttg atgactggc cttatgcctt 600
 tgagcgggga gacaatccct ttcccaagaa tgccgatgga actgtcagat atgactcaac 660
 tcactataaa gagacctgga aggctctgga ggtactggtg gcaaaggggc tgggtgaaagc 720
 cctgggcttg tccaacttca acagtcggca gattgatgat gtccctcagt tggcctctgt 780
 ggcgccagct gtcttgccagg tggaatgccca tccatacctg gctcagaatg agctcattgc 840
 ccactgtcac gcacggggct tggaggtgac tgcttatagc cccttgggtt cctctgaccg 900
 tgcttggcgc catcctgatg agccagtcct gcttgaagaa ccagtagtct tggcactagc 960
 tgaaaaacat ggccgatctc cagctcagat cttgcttaga tggcaggttc agcggaaggt 1020
 gatctgcac cccaaaagca tcaatccttc ccgcacctt cagaacattc aggtatttga 1080
 tttcaccttt agcccagagg agatgaaaca attagatgct ctgaacaaaa attggcggta 1140
 tattgtgccc atgattacgg tggatgggaa gaggggtccc agagatgctg gacaccctct 1200
 gtatcccttt aatgacccat actgagacct atagtttctc agcttccctt tcagttctcc 1260
 tgctaagcat tgctgtctac tccccagaaa gaaggaatca ataaagccat tgaagtgtaa 1320

<210> 76
 <211> 325
 <212> PRT
 <213> Mus musculus

<220>
 <223> mouse aldo-keto reductase family 1, member A4
 (aldehyde reductase) (Akrla4)

<400> 76
 Met Thr Ala Ser Ser Val Leu Leu His Thr Gly Gln Lys Met Pro Leu
 1 5 10 15
 Ile Gly Leu Gly Thr Trp Lys Ser Glu Pro Gly Gln Val Lys Ala Ala
 20 25 30
 Ile Lys His Ala Leu Ser Ala Gly Tyr Arg His Ile Asp Cys Ala Ser
 35 40 45
 Val Tyr Gly Asn Glu Thr Glu Ile Gly Glu Ala Leu Lys Glu Ser Val
 50 55 60

Gly Ser Gly Lys Ala Val Pro Arg Glu Glu Leu Phe Val Thr Ser Lys
 65 70 75 80
 Leu Trp Asn Thr Lys His His Pro Glu Asp Val Glu Pro Ala Leu Arg
 85 90 95
 Lys Thr Leu Ala Asp Leu Gln Leu Glu Tyr Leu Asp Leu Tyr Leu Met
 100 105 110
 His Trp Pro Tyr Ala Phe Glu Arg Gly Asp Asn Pro Phe Pro Lys Asn
 115 120 125
 Ala Asp Gly Thr Val Arg Tyr Asp Ser Thr His Tyr Lys Glu Thr Trp
 130 135 140
 Lys Ala Leu Glu Val Leu Val Ala Lys Gly Leu Val Lys Ala Leu Gly
 145 150 155 160
 Leu Ser Asn Phe Asn Ser Arg Gln Ile Asp Asp Val Leu Ser Val Ala
 165 170 175
 Ser Val Arg Pro Ala Val Leu Gln Val Glu Cys His Pro Tyr Leu Ala
 180 185 190
 Gln Asn Glu Leu Ile Ala His Cys His Ala Arg Gly Leu Glu Val Thr
 195 200 205
 Ala Tyr Ser Pro Leu Gly Ser Ser Asp Arg Ala Trp Arg His Pro Asp
 210 215 220
 Glu Pro Val Leu Leu Glu Glu Pro Val Val Leu Ala Leu Ala Glu Lys
 225 230 235 240
 His Gly Arg Ser Pro Ala Gln Ile Leu Leu Arg Trp Gln Val Gln Arg
 245 250 255
 Lys Val Ile Cys Ile Pro Lys Ser Ile Asn Pro Ser Arg Ile Leu Gln
 260 265 270
 Asn Ile Gln Val Phe Asp Phe Thr Phe Ser Pro Glu Glu Met Lys Gln
 275 280 285
 Leu Asp Ala Leu Asn Lys Asn Trp Arg Tyr Ile Val Pro Met Ile Thr
 290 295 300
 Val Asp Gly Lys Arg Val Pro Arg Asp Ala Gly His Pro Leu Tyr Pro
 305 310 315 320
 Phe Asn Asp Pro Tyr
 325

<210> 77

<211> 1124

<212> DNA

<213> Rattus norvegicus

<220>

<223> rat aldo-keto reductase family 1, member A1
 (aldehyde reductase) (Akrla1) cDNA

<220>
 <221> CDS
 <222> (54)..(1031)
 <223> aldehyde reductase

<400> 77
 gaattctggc cactttgtct tctccacagc ctgtgctcat tgccaagggg acaatgacgg 60
 cctccagtgt cctcctgcac actggacaga agatgcctct gattgggtctg gggacatgga 120
 agagtgagcc tggtcagggtg aaagcagcta ttaaatatgc ccttagcgta ggctaccgcc 180
 acattgactg tgctttctgta tatggcaatg aaactgagat tggagaggcc ctgaaggaga 240
 gtgtggggagc aggcaaggca gtacctcgag aggagctgtt tgtgacctcc aagctgtgga 300
 atactaagca ccaccctgag gatgtagaac ctgctgtccg gaagacgctg gctgatctgc 360
 agctggagta tttggacctc tatttgatgc attggcctta tgccttcgag cggggagaca 420
 atccctttcc caagaatgcc gatggaactg tcaaatatga ctccactcac tataaggaga 480
 cctggaaggc tctggaggca ctggtggcaa aggggctggt gaaagccttg ggcttgtcca 540
 acttcagcag tcggcagata gatgatgtcc tcagtgtggc ctcggtgcgc ccagctgtct 600
 tgcaggtgga atgccatcca tacctggctc aaaatgagct cattgcccac tgtcaagcac 660
 gaggcttgga ggtgacagct tacagcccct tgggttcacg ggatcggtgct tggcgccacc 720
 ctgatgagcc agtcctgctt gaggaaccag ttgtcttggc actagctgaa aaacatggcc 780
 gatctccagc tcagatcttg ctcatatggc aggttcagcg gaaagtaatc tgcattccca 840
 aaagcatcac tccttcccgc atccttcaga acattcaggt atttgatttc acctttagtc 900
 cagaggagat gaagcaatta gatgctctga acaaaaattg gcggtatatt gtgcccatga 960
 ttacgggtgga tgggaagaga gtccccagag atgctggaca cctctgtat ccctttaatg 1020
 acccatactg aggcccgtag tttctcagct tccctttcag ttctcctgct aagcattgcc 1080
 tgctactccc aagaaagaag gactcaataa agccattgaa gtgt 1124

<210> 78
 <211> 325
 <212> PRT
 <213> Rattus norvegicus

<220>
 <223> rat aldo-keto reductase family 1, member A1
 (aldehyde reductase) (Akrla1)

<400> 78
 Met Thr Ala Ser Ser Val Leu Leu His Thr Gly Gln Lys Met Pro Leu
 1 5 10 15
 Ile Gly Leu Gly Thr Trp Lys Ser Glu Pro Gly Gln Val Lys Ala Ala
 20 25 30
 Ile Lys Tyr Ala Leu Ser Val Gly Tyr Arg His Ile Asp Cys Ala Ser
 35 40 45
 Val Tyr Gly Asn Glu Thr Glu Ile Gly Glu Ala Leu Lys Glu Ser Val
 50 55 60
 Gly Ala Gly Lys Ala Val Pro Arg Glu Glu Leu Phe Val Thr Ser Lys
 65 70 75 80
 Leu Trp Asn Thr Lys His His Pro Glu Asp Val Glu Pro Ala Val Arg
 85 90 95
 Lys Thr Leu Ala Asp Leu Gln Leu Glu Tyr Leu Asp Leu Tyr Leu Met
 100 105 110
 His Trp Pro Tyr Ala Phe Glu Arg Gly Asp Asn Pro Phe Pro Lys Asn
 115 120 125

Ala Asp Gly Thr Val Lys Tyr Asp Ser Thr His Tyr Lys Glu Thr Trp
 130 135 140
 Lys Ala Leu Glu Ala Leu Val Ala Lys Gly Leu Val Lys Ala Leu Gly
 145 150 155 160
 Leu Ser Asn Phe Ser Ser Arg Gln Ile Asp Asp Val Leu Ser Val Ala
 165 170 175
 Ser Val Arg Pro Ala Val Leu Gln Val Glu Cys His Pro Tyr Leu Ala
 180 185 190
 Gln Asn Glu Leu Ile Ala His Cys Gln Ala Arg Gly Leu Glu Val Thr
 195 200 205
 Ala Tyr Ser Pro Leu Gly Ser Ser Asp Arg Ala Trp Arg His Pro Asp
 210 215 220
 Glu Pro Val Leu Leu Glu Glu Pro Val Val Leu Ala Leu Ala Glu Lys
 225 230 235 240
 His Gly Arg Ser Pro Ala Gln Ile Leu Leu Arg Trp Gln Val Gln Arg
 245 250 255
 Lys Val Ile Cys Ile Pro Lys Ser Ile Thr Pro Ser Arg Ile Leu Gln
 260 265 270
 Asn Ile Gln Val Phe Asp Phe Thr Phe Ser Pro Glu Glu Met Lys Gln
 275 280 285
 Leu Asp Ala Leu Asn Lys Asn Trp Arg Tyr Ile Val Pro Met Ile Thr
 290 295 300
 Val Asp Gly Lys Arg Val Pro Arg Asp Ala Gly His Pro Leu Tyr Pro
 305 310 315 320
 Phe Asn Asp Pro Tyr
 325

<210> 79

<211> 3871

<212> DNA

<213> Homo sapiens

<220>

<223> human phosphodiesterase 4B (PDE4B) cDNA

<220>

<221> CDS

<222> (282)..(1976)

<223> PDE4B

<400> 79

ggcacgagcc taaagaaccc tgggatgact aaggcagaga gagtctgaga aaactctttg 60
 gtgcttctgc ctttagtttt aggacacatt tatgcagatg agcttataag agaccgttcc 120
 ctccgccttc ttcctcagag gaagtttctt ggtagatcac cgacacctca tccaggcggg 180
 ggggtggggg gaaacttggc accagccatc ccaggcagag caccactgtg atttgttctc 240
 ctggtgggag gagctggaag gaaggagcca gcgtgcaaata atgaaggag cacgggggca 300
 ccttcagtag caccggaatc agcgggtggtg gcggtgactc tgctatggac agcctgcagc 360
 cgctccagcc taactacatg cctgtgtgtt tgtttgcaga agaattctat caaaaattag 420

caatggaaac	gctggaggaa	ttagactggt	gttttagacca	gctagagacc	atacagacct	480
accggtctgt	cagtgaagatg	gcttctaaca	agttcaaaaag	aatgctgaac	cgggagctga	540
cacacctctc	agagatgagc	cgatcagggg	accaggtgtc	tgaatacatt	tcaaataactt	600
tcttagacaa	gcagaatgat	gtggagatcc	catctcctac	ccagaaaagac	agggagaaaa	660
agaaaaagca	gcagctcatg	acccagataa	gtggagtga	gaaattaatg	catagttcaa	720
gcctaaacaa	tacaagcatc	tcacgctttg	gagtcaacac	tgaaaatgaa	gatcacctgg	780
ccaaggagct	ggaagacctg	aacaaatggg	gtcttaacat	ctttaatgtg	gctggatatt	840
ctcacaatag	accctaaca	tgcatcatgt	atgctatatt	ccaggaaaga	gacctcctaa	900
agacattcag	aatctcatct	gacacattta	taacctacat	gatgacttta	gaagaccatt	960
accatttctga	cgtggcatat	cacaacagcc	tgcacgctgc	tgatgtagcc	cagtcgaccc	1020
atgtttctct	ttctacacca	gcattagacg	ctgtcttcac	agatttggag	atcctggctg	1080
ccatttttgc	agctgccatc	catgacgttg	atcactcctg	agtctccaat	cagtttctca	1140
tcaacacaaa	ttcagaactt	gctttgatgt	ataatgatga	atctgtgttg	gaaaatcatt	1200
accttgctgt	gggtttcaaa	ctgctgcaag	aagaacactg	tgacatcttc	atgaatctca	1260
ccaagaagca	gcgtcagaca	ctcaggaaga	tggttattga	catggtgtta	gcaactgata	1320
tgtctaaaca	tatgagcctg	ctggcagacc	tgaagacaat	ggtagaaacg	aagaaagtta	1380
caagttcagg	cgttcttctc	ctagacaact	ataccgatcg	cattcagggtc	cttcgcaaca	1440
tggtacactg	tgcagacctg	agcaacccca	ccaagtcctt	ggaattgtat	cggcaatgga	1500
cagaccgcat	catggaggaa	tttttccagc	agggagacaa	agagcgggag	aggggaatgg	1560
aaattagccc	aatgtgtgat	aaacacacag	cttctgtgga	aaaatcccag	gttggtttca	1620
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aggacattct	cgatacctta	gaagataaca	ggaactggta	tcagagcatg	atacctcaaa	1740
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agtttgaact	gactctcgat	gaggaagatt	ctgaaggacc	tgagaaggag	ggagagggac	1860
acagctatct	cagcagcaca	aagacgcttt	gtgtgattga	tccagaaaac	agagattccc	1920
tggtgagagc	tgacatagac	attgcaacag	aagacaagtc	ccccgtggat	acataatccc	1980
cctctccctg	tggagatgaa	cattctatcc	ttgatgagca	tgccagctat	gtggtagggc	2040
cagcccacca	tgggggcca	gacctgcaca	ggacaagggc	cacctggctt	tcagttactt	2100
gagtttggag	tcagaaaagca	agaccaggaa	gcaaatagca	gctcaggaaa	ttccacgggt	2160
gacttgcctt	gatggcaagc	ttggtggaga	gggctgaagc	tggtgctggg	ggccgattct	2220
gatcaagaca	catggcttga	aaatggaaga	cacaaaactg	agagatcatt	ctgcactaag	2280
tttcgggaac	ttatccccga	cagtgaactga	actcactgac	taataacttc	atztatgaat	2340
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ctttaaaatg	cctgttgaat	acctggagtt	tagtatcaac	ttctacacag	ataagctttc	2460
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cttctaacca	catttttactt	ccttccccctg	ttgtccagtc	caactccaca	gtcactctta	2640
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ctgccgtcct	tctcttgcac	tgcccttctgc	gctaacacct	ccattcctgt	ttataaccgt	2940
gtatttatta	cttaatgtat	ataatgtaat	gttttgtaag	ttattaattt	atatacttaa	3000
cattgcctgc	caatgggtgg	gttaaatttg	tgtagaaaac	tctgcctaag	agttacgact	3060
ttttcttgta	atgttttgta	ttgtgtatta	tataacccaa	acgtcactta	gtagagacat	3120
atggccccct	tggcagagag	gacaggggtg	ggcttttgtt	caaagggctt	gccctttccc	3180
tgcttgagtt	gctacttctg	cacaacccct	ttatgaacca	gttttggaaa	caatattcta	3240
cacattagat	actaaatggg	ttatactgag	cttttacttt	tgatatagctt	gataggggca	3300
gggggcaatg	gatgtagtgt	ttacccaggt	tctatccaaa	tctatgtggg	catgagttgg	3360
gttataactg	gatacctacta	tcattgtggc	tttggttcaa	aaggaaaacac	tacatttgct	3420
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aatttttata	ataaaatgtg	aactgatgta	gcaaattacg	caaagtgtgaa	gcctcttctg	3600
ataacacttg	ttaggcctct	tactgatgtc	agtttcagtt	tgtaaaatat	gtttcatgct	3660
ttcagttcag	cattgtgact	cagtaaatac	agaaaatggc	acaaatgtgc	atgaccaatg	3720
tatgtctatg	aacactgcat	tgtttcaggt	ggacatttta	tcgattttca	aatgtttctc	3780
acaatgtatg	ttatagtgtt	attattatat	attgtgttca	aatgcattct	aaagagactt	3840
ttatatgagg	tgaataaaga	aaagcataat	t			3871

<210> 80
 <211> 564
 <212> PRT
 <213> Homo sapiens

<220>
 <223> human phosphodiesterase 4B (PDE4B)

<400> 80
 Met Lys Glu His Gly Gly Thr Phe Ser Ser Thr Gly Ile Ser Gly Gly
 1 5 10 15
 Ser Gly Asp Ser Ala Met Asp Ser Leu Gln Pro Leu Gln Pro Asn Tyr
 20 25 30
 Met Pro Val Cys Leu Phe Ala Glu Glu Ser Tyr Gln Lys Leu Ala Met
 35 40 45
 Glu Thr Leu Glu Glu Leu Asp Trp Cys Leu Asp Gln Leu Glu Thr Ile
 50 55 60
 Gln Thr Tyr Arg Ser Val Ser Glu Met Ala Ser Asn Lys Phe Lys Arg
 65 70 75 80
 Met Leu Asn Arg Glu Leu Thr His Leu Ser Glu Met Ser Arg Ser Gly
 85 90 95
 Asn Gln Val Ser Glu Tyr Ile Ser Asn Thr Phe Leu Asp Lys Gln Asn
 100 105 110
 Asp Val Glu Ile Pro Ser Pro Thr Gln Lys Asp Arg Glu Lys Lys Lys
 115 120 125
 Lys Gln Gln Leu Met Thr Gln Ile Ser Gly Val Lys Lys Leu Met His
 130 135 140
 Ser Ser Ser Leu Asn Asn Thr Ser Ile Ser Arg Phe Gly Val Asn Thr
 145 150 155 160
 Glu Asn Glu Asp His Leu Ala Lys Glu Leu Glu Asp Leu Asn Lys Trp
 165 170 175
 Gly Leu Asn Ile Phe Asn Val Ala Gly Tyr Ser His Asn Arg Pro Leu
 180 185 190
 Thr Cys Ile Met Tyr Ala Ile Phe Gln Glu Arg Asp Leu Leu Lys Thr
 195 200 205
 Phe Arg Ile Ser Ser Asp Thr Phe Ile Thr Tyr Met Met Thr Leu Glu
 210 215 220
 Asp His Tyr His Ser Asp Val Ala Tyr His Asn Ser Leu His Ala Ala
 225 230 235 240
 Asp Val Ala Gln Ser Thr His Val Leu Leu Ser Thr Pro Ala Leu Asp
 245 250 255
 Ala Val Phe Thr Asp Leu Glu Ile Leu Ala Ala Ile Phe Ala Ala Ala
 260 265 270

<220>
 <223> mouse phosphodiesterase 4B (PDE4B) cDNA

<220>
 <221> CDS
 <222> (23)..(2188)
 <223> PDE4B

<400> 81
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 aaagctacca ggaaacagac ctacatctcc caaaatttct ccacgcagtt caccaaggaa 180
 ttcaccatgc tttttcagaa agttgctggt gaataaaagc atccgacagc ggcgtcgctt 240
 cacgggtggct catacatgct ttgatgtgga aaatggccct tctccagggtc ggagcccact 300
 ggaccctcaa gccggctctt cgtcgggact ggtacttcat gccgcctttc ctgggcacag 360
 ccagcgcagg gagtcgttcc tctacagatc tgacagcgac tatgacttgt caccaaaagc 420
 gatgtccagg aactcatcac ttcccagtg gcaacacggc gatgacctga ttgtcactcc 480
 ttttgcccag gttcttgcca gcttgccaag tgtaagaaac aacttcaccc tgctgacgaa 540
 ccttcatgga gcgccgaaca agaggtcacc agcggctagt caggctccag tctccagagt 600
 cagcctgcaa gaagaatcat atcagaaact agcaatggag acgctggagg aactagactg 660
 gtgcctagac cagctagaga ccattccagac ctaccgctct gtcagcgaga tggcttcaaa 720
 caagttcaaa aggatgctga accgggagct gacacacctc tcagagatga gcagatcagg 780
 gaaccagggtg tctgagtaca tttcaaacac gttcttagac aagcagaacg atgtggaaat 840
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 cggagtcaac acggaaaatg aggatcatct agccaaggag ctggaagacc tgaacaaatg 1020
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 tgtaacctac atgatgactt tagaagacca ttaccattct gatgtggcat atcacaacag 1200
 cctgcatgct gctgacgtgg ccagtcacac tcacgttctc ctttctacgc cggcactgga 1260
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 cgatcatcct ggagtctcca atcagtttct catcaataca aattctgaac ttgctttgat 1380
 gtataatgat gaatctgttc tggaaaacca tcaccttgct gtgggattca aattgctaca 1440
 agaggaacac tgcgacatct ttcagaatct taccaagaag caacgccaga cactcaggaa 1500
 aatggtgatt gacatggtgt tggcaactga tatgtccaaa cacatgagcc tcctggcaga 1560
 ccttaaaaca atggtagaaa ccaagaagggt gacaagctcc ggtgttctcc tcctggacaa 1620
 ctatactgac cggatacagg ttcttcgcaa catggtacac tgtgcagacc tgagcaacct 1680
 caccaagtcc ttggaattgt atcggcaatg gaccgatcgt atcatggagg agtttttcca 1740
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 agcttctgtg gaaaaatccc aggttggttt cattgactac attgtccatc cactgtggga 1860
 gacctgggca gacctggttc aaccggatgc tcaagatatt ctggatacac tagaagataa 1920
 caggaactgg taccagagta tgatacccca gagcccttcc ccgccactgg atgagaggag 1980
 cagggactgc caaggcctga tggagaagtt tcagtttgaa ctgacccttg aggaagagga 2040
 ttctgaggga ccggaaaagg agggagaagg ccacagctat ttcagcagca caaagacgct 2100
 ttgtgtgatt gatccagaga acagggattc tctggaagag actgacatag acattgcaac 2160
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 acccttgact gagca 2235

<210> 82
 <211> 721
 <212> PRT
 <213> Mus musculus

<220>
 <223> mouse phosphodiesterase 4B (PDE4B)

<400> 82
 Met Thr Ala Lys Asn Ser Pro Lys Glu Phe Thr Ala Ser Glu Ser Glu
 1 5 10 15

Val Cys Ile Lys Thr Phe Lys Glu Gln Met Arg Leu Glu Leu Glu Leu
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Pro Lys Leu Pro Gly Asn Arg Pro Thr Ser Pro Lys Ile Ser Pro Arg
35 40 45
Ser Ser Pro Arg Asn Ser Pro Cys Phe Phe Arg Lys Leu Leu Val Asn
50 55 60
Lys Ser Ile Arg Gln Arg Arg Arg Phe Thr Val Ala His Thr Cys Phe
65 70 75 80
Asp Val Glu Asn Gly Pro Ser Pro Gly Arg Ser Pro Leu Asp Pro Gln
85 90 95
Ala Gly Ser Ser Ser Gly Leu Val Leu His Ala Ala Phe Pro Gly His
100 105 110
Ser Gln Arg Arg Glu Ser Phe Leu Tyr Arg Ser Asp Ser Asp Tyr Asp
115 120 125
Leu Ser Pro Lys Ala Met Ser Arg Asn Ser Ser Leu Pro Ser Glu Gln
130 135 140
His Gly Asp Asp Leu Ile Val Thr Pro Phe Ala Gln Val Leu Ala Ser
145 150 155 160
Leu Arg Ser Val Arg Asn Asn Phe Thr Leu Leu Thr Asn Leu His Gly
165 170 175
Ala Pro Asn Lys Arg Ser Pro Ala Ala Ser Gln Ala Pro Val Ser Arg
180 185 190
Val Ser Leu Gln Glu Glu Ser Tyr Gln Lys Leu Ala Met Glu Thr Leu
195 200 205
Glu Glu Leu Asp Trp Cys Leu Asp Gln Leu Glu Thr Ile Gln Thr Tyr
210 215 220
Arg Ser Val Ser Glu Met Ala Ser Asn Lys Phe Lys Arg Met Leu Asn
225 230 235 240
Arg Glu Leu Thr His Leu Ser Glu Met Ser Arg Ser Gly Asn Gln Val
245 250 255
Ser Glu Tyr Ile Ser Asn Thr Phe Leu Asp Lys Gln Asn Asp Val Glu
260 265 270
Ile Pro Ser Pro Thr Gln Lys Asp Arg Glu Lys Lys Lys Lys Gln Gln
275 280 285
Leu Met Thr Gln Ile Ser Gly Val Lys Lys Leu Met His Ser Ser Ser
290 295 300
Leu Asn Asn Thr Ser Ile Ser Arg Phe Gly Val Asn Thr Glu Asn Glu
305 310 315 320
Asp His Leu Ala Lys Glu Leu Glu Asp Leu Asn Lys Trp Gly Leu Asn
325 330 335

Ile	Phe	Asn	Val	Ala	Gly	Tyr	Ser	His	Asn	Arg	Pro	Leu	Thr	Cys	Ile	340	345	350	
Met	Tyr	Ala	Ile	Phe	Gln	Glu	Arg	Asp	Leu	Leu	Lys	Thr	Phe	Lys	Ile	355	360	365	
Ser	Ser	Asp	Thr	Phe	Val	Thr	Tyr	Met	Met	Thr	Leu	Glu	Asp	His	Tyr	370	375	380	
His	Ser	Asp	Val	Ala	Tyr	His	Asn	Ser	Leu	His	Ala	Ala	Asp	Val	Ala	385	390	395	400
Gln	Ser	Thr	His	Val	Leu	Leu	Ser	Thr	Pro	Ala	Leu	Asp	Ala	Val	Phe	405	410	415	
Thr	Asp	Leu	Glu	Ile	Leu	Ala	Ala	Ile	Phe	Ala	Ala	Ala	Ile	His	Asp	420	425	430	
Val	Asp	His	Pro	Gly	Val	Ser	Asn	Gln	Phe	Leu	Ile	Asn	Thr	Asn	Ser	435	440	445	
Glu	Leu	Ala	Leu	Met	Tyr	Asn	Asp	Glu	Ser	Val	Leu	Glu	Asn	His	His	450	455	460	
Leu	Ala	Val	Gly	Phe	Lys	Leu	Leu	Gln	Glu	Glu	His	Cys	Asp	Ile	Phe	465	470	475	480
Gln	Asn	Leu	Thr	Lys	Lys	Gln	Arg	Gln	Thr	Leu	Arg	Lys	Met	Val	Ile	485	490	495	
Asp	Met	Val	Leu	Ala	Thr	Asp	Met	Ser	Lys	His	Met	Ser	Leu	Leu	Ala	500	505	510	
Asp	Leu	Lys	Thr	Met	Val	Glu	Thr	Lys	Lys	Val	Thr	Ser	Ser	Gly	Val	515	520	525	
Leu	Leu	Leu	Asp	Asn	Tyr	Thr	Asp	Arg	Ile	Gln	Val	Leu	Arg	Asn	Met	530	535	540	
Val	His	Cys	Ala	Asp	Leu	Ser	Asn	Pro	Thr	Lys	Ser	Leu	Glu	Leu	Tyr	545	550	555	560
Arg	Gln	Trp	Thr	Asp	Arg	Ile	Met	Glu	Glu	Phe	Phe	Gln	Gln	Gly	Asp	565	570	575	
Lys	Glu	Arg	Glu	Arg	Gly	Met	Glu	Ile	Ser	Pro	Met	Cys	Asp	Lys	His	580	585	590	
Thr	Ala	Ser	Val	Glu	Lys	Ser	Gln	Val	Gly	Phe	Ile	Asp	Tyr	Ile	Val	595	600	605	
His	Pro	Leu	Trp	Glu	Thr	Trp	Ala	Asp	Leu	Val	Gln	Pro	Asp	Ala	Gln	610	615	620	
Asp	Ile	Leu	Asp	Thr	Leu	Glu	Asp	Asn	Arg	Asn	Trp	Tyr	Gln	Ser	Met	625	630	635	640
Ile	Pro	Gln	Ser	Pro	Ser	Pro	Pro	Leu	Asp	Glu	Arg	Ser	Arg	Asp	Cys	645	650	655	

Gln Gly Leu Met Glu Lys Phe Gln Phe Glu Leu Thr Leu Glu Glu Glu
660 665 670

Asp Ser Glu Gly Pro Glu Lys Glu Gly Glu Gly His Ser Tyr Phe Ser
675 680 685

Ser Thr Lys Thr Leu Cys Val Ile Asp Pro Glu Asn Arg Asp Ser Leu
690 695 700

Glu Glu Thr Asp Ile Asp Ile Ala Thr Glu Asp Lys Ser Pro Ile Asp
705 710 715 720

Thr

<210> 83
<211> 2647
<212> DNA
<213> Rattus norvegicus

<220>
<223> rat phosphodiesterase 4B (PDE4B) cDNA

<220>
<221> CDS
<222> (542)..(2236)
<223> PDE4B

<400> 83
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acctgaagca tttttcccca gaatgaatga ctgccctgcc tgagaacaga agagccaaac 180
agttcccccc acatggccat agggagctgg tttcatttag aagaaaagca aagagagggg 240
aaagcctccc tcatttctcc tccggacggc aaacattcag aaatgacatc acacacccca 300
cagccccggg atgactaagg cagaagtagc ctgagaaaac tctgctctgc cctgagtttt 360
agggcacagt tatgcagatg agcgtctggg cgcaggttcc cgccttcttc ctctgaggaa 420
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<210> 84
<211> 564
<212> PRT
<213> Rattus norvegicus

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<220>
<223> rat phosphodiesterase 4B (PDE4B)

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<400> 84
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Gly Gly Asp Ser Ala Met Ala Ser Leu Gln Pro Leu Gln Pro Asn Tyr
          20                      25                      30

Leu Ser Val Cys Leu Phe Ala Glu Glu Ser Tyr Gln Lys Leu Ala Met
          35                      40                      45

Glu Thr Leu Glu Glu Leu Asp Trp Cys Leu Asp Gln Leu Glu Thr Ile
  50                      55                      60

Gln Thr Tyr Arg Ser Val Ser Glu Met Ala Ser Asn Lys Phe Lys Arg
  65                      70                      75                      80

Met Leu Asn Arg Glu Leu Thr His Leu Ser Glu Met Ser Arg Ser Gly
          85                      90                      95

Asn Gln Val Ser Glu Tyr Ile Ser Asn Thr Phe Leu Asp Lys Gln Asn
          100                     105                     110

Asp Val Glu Ile Pro Ser Pro Thr Gln Lys Asp Arg Glu Lys Lys Lys
          115                     120                     125

Lys Gln Gln Leu Met Thr Gln Ile Ser Gly Val Lys Lys Leu Met His
          130                     135                     140

Ser Ser Ser Leu Asn Asn Thr Ser Ile Ser Arg Phe Gly Val Asn Thr
          145                     150                     155                     160

Glu Asn Glu Asp His Leu Ala Lys Glu Leu Glu Asp Leu Asn Lys Trp
          165                     170                     175

Gly Leu Asn Ile Phe Asn Val Ala Gly Tyr Ser His Asn Arg Pro Leu
          180                     185                     190

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Thr	Cys	Ile	Met	Tyr	Ala	Ile	Phe	Gln	Glu	Arg	Asp	Leu	Leu	Lys	Thr	195	200	205
Phe	Lys	Ile	Ser	Ser	Asp	Thr	Phe	Val	Thr	Tyr	Met	Met	Thr	Leu	Glu	210	215	220
Asp	His	Tyr	His	Ser	Asp	Val	Ala	Tyr	His	Asn	Ser	Leu	His	Ala	Ala	225	230	235
Asp	Val	Ala	Gln	Ser	Thr	His	Val	Leu	Leu	Ser	Thr	Pro	Ala	Leu	Asp	245	250	255
Ala	Val	Phe	Thr	Asp	Leu	Glu	Ile	Leu	Ala	Ala	Ile	Phe	Ala	Ala	Ala	260	265	270
Ile	His	Asp	Val	Asp	His	Pro	Gly	Val	Ser	Asn	Gln	Phe	Leu	Ile	Asn	275	280	285
Thr	Asn	Ser	Glu	Leu	Ala	Leu	Met	Tyr	Asn	Asp	Glu	Ser	Val	Leu	Glu	290	295	300
Asn	His	His	Leu	Ala	Val	Gly	Phe	Lys	Leu	Leu	Gln	Glu	Glu	His	Cys	305	310	315
Asp	Ile	Phe	Gln	Asn	Leu	Thr	Lys	Lys	Gln	Arg	Gln	Thr	Leu	Arg	Lys	325	330	335
Met	Val	Ile	Asp	Met	Val	Leu	Ala	Thr	Asp	Met	Ser	Lys	His	Met	Ser	340	345	350
Leu	Leu	Ala	Asp	Leu	Lys	Thr	Met	Val	Glu	Thr	Lys	Lys	Val	Thr	Ser	355	360	365
Ser	Gly	Val	Leu	Leu	Leu	Asp	Asn	Tyr	Thr	Asp	Arg	Ile	Gln	Val	Leu	370	375	380
Arg	Asn	Met	Val	His	Cys	Ala	Asp	Leu	Ser	Asn	Pro	Thr	Lys	Ser	Leu	385	390	395
Glu	Leu	Tyr	Arg	Gln	Trp	Thr	Asp	Arg	Ile	Met	Glu	Glu	Phe	Phe	Gln	405	410	415
Gln	Gly	Asp	Lys	Glu	Arg	Glu	Arg	Gly	Met	Glu	Ile	Ser	Pro	Met	Cys	420	425	430
Asp	Lys	His	Thr	Ala	Ser	Val	Glu	Lys	Ser	Gln	Val	Gly	Phe	Ile	Asp	435	440	445
Tyr	Ile	Val	His	Pro	Leu	Trp	Glu	Thr	Trp	Ala	Asp	Leu	Val	Gln	Pro	450	455	460
Asp	Ala	Gln	Asp	Ile	Leu	Asp	Thr	Leu	Glu	Asp	Asn	Arg	Asn	Trp	Tyr	465	470	475
Gln	Ser	Met	Ile	Pro	Gln	Ser	Pro	Ser	Pro	Pro	Leu	Asp	Glu	Arg	Ser	485	490	495
Arg	Asp	Cys	Gln	Gly	Leu	Met	Glu	Lys	Phe	Gln	Phe	Glu	Leu	Thr	Leu	500	505	510

Glu Glu Glu Asp Ser Glu Gly Pro Glu Lys Glu Gly Glu Gly Pro Asn
515 520 525

Tyr Phe Ser Ser Thr Lys Thr Leu Cys Val Ile Asp Pro Glu Asn Arg
530 535 540

Asp Ser Leu Glu Glu Thr Asp Ile Asp Ile Ala Thr Glu Asp Lys Ser
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Leu Ile Asp Thr

<210> 85
<211> 1880
<212> DNA
<213> Homo sapiens

<220>
<223> human sterol 27-dehydrogenase (CYP27) cDNA

<220>
<221> CDS
<222> (22) .. (1617)
<223> CYP27

<400> 85
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gccctcccct cggacaaggc caccggagct cccggagccg ggcctggtgt ccggcggcgg 180
caacggagct tagaggagat tccacgtcta ggacagctgc gcttcttctt tcagctgttc 240
gttcaaggct atgccctgca actgcaccag ttacaggtgc tttacaaggc caagtacggg 300
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aaggagcacc gggaccagca cgacctgacc tatgggcccgt tcaccacgga aggacaccac 480
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cccaggaca ccgtgacctt cgtcagatcc atcgggttaa tgttccagaa ctactctat 780
gccaccttc tcccccaagt gactcgcccc gtgtgcctt tctggaagcg atacctggat 840
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cagcctgcta cccccaggat ccagacccca tttggctctg tgcccttttg ctatgggggtc 1440
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<210> 86
 <211> 531
 <212> PRT
 <213> Homo sapiens

 <220>
 <223> human sterol 27-dehydrogenase (CYP27)

 <400> 86
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 20 25 30
 Ala Ala Leu Pro Ser Asp Lys Ala Thr Gly Ala Pro Gly Ala Gly Pro
 35 40 45
 Gly Val Arg Arg Arg Gln Arg Ser Leu Glu Glu Ile Pro Arg Leu Gly
 50 55 60
 Gln Leu Arg Phe Phe Phe Gln Leu Phe Val Gln Gly Tyr Ala Leu Gln
 65 70 75 80
 Leu His Gln Leu Gln Val Leu Tyr Lys Ala Lys Tyr Gly Pro Met Trp
 85 90 95
 Met Ser Tyr Leu Gly Pro Gln Met His Val Asn Leu Ala Ser Ala Pro
 100 105 110
 Leu Leu Glu Gln Val Met Arg Gln Glu Gly Lys Tyr Pro Val Arg Asn
 115 120 125
 Asp Met Glu Leu Trp Lys Glu His Arg Asp Gln His Asp Leu Thr Tyr
 130 135 140
 Gly Pro Phe Thr Thr Glu Gly His His Trp Tyr Gln Leu Arg Gln Ala
 145 150 155 160
 Leu Asn Gln Arg Leu Leu Lys Pro Ala Glu Ala Ala Leu Tyr Thr Asp
 165 170 175
 Ala Phe Asn Glu Val Ile Asp Asp Phe Met Thr Arg Leu Asp Gln Leu
 180 185 190
 Arg Ala Glu Ser Ala Ser Gly Asn Gln Val Ser Asp Met Ala Gln Leu
 195 200 205
 Phe Tyr Tyr Phe Ala Leu Glu Ala Ile Cys Tyr Ile Leu Phe Glu Lys
 210 215 220
 Arg Ile Gly Cys Leu Gln Arg Ser Ile Pro Glu Asp Thr Val Thr Phe
 225 230 235 240
 Val Arg Ser Ile Gly Leu Met Phe Gln Asn Ser Leu Tyr Ala Thr Phe
 245 250 255
 Leu Pro Lys Trp Thr Arg Pro Val Leu Pro Phe Trp Lys Arg Tyr Leu
 260 265 270

Asp Gly Trp Asn Ala Ile Phe Ser Phe Gly Lys Lys Leu Ile Asp Glu
 275 280 285
 Lys Leu Glu Asp Met Glu Ala Gln Leu Gln Ala Ala Gly Pro Asp Gly
 290 295 300
 Ile Gln Val Ser Gly Tyr Leu His Phe Leu Leu Ala Ser Gly Gln Leu
 305 310 315 320
 Ser Pro Arg Glu Ala Met Gly Ser Leu Pro Glu Leu Leu Met Ala Gly
 325 330 335
 Val Asp Thr Thr Ser Asn Thr Leu Thr Trp Ala Leu Tyr His Leu Ser
 340 345 350
 Lys Asp Pro Glu Ile Gln Glu Ala Leu His Glu Glu Val Val Gly Val
 355 360 365
 Val Pro Ala Gly Gln Val Pro Gln His Lys Asp Phe Ala His Met Pro
 370 375 380
 Leu Leu Lys Ala Val Leu Lys Glu Thr Leu Arg Leu Tyr Pro Val Val
 385 390 395 400
 Pro Thr Asn Ser Arg Ile Ile Glu Lys Glu Ile Glu Val Asp Gly Phe
 405 410 415
 Leu Phe Pro Lys Asn Thr Gln Phe Val Phe Cys His Tyr Val Val Ser
 420 425 430
 Arg Asp Pro Thr Ala Phe Ser Glu Pro Glu Ser Phe Gln Pro His Arg
 435 440 445
 Trp Leu Arg Asn Ser Gln Pro Ala Thr Pro Arg Ile Gln His Pro Phe
 450 455 460
 Gly Ser Val Pro Phe Gly Tyr Gly Val Arg Ala Cys Leu Gly Arg Arg
 465 470 475 480
 Ile Ala Glu Leu Glu Met Gln Leu Leu Leu Ala Arg Leu Ile Gln Lys
 485 490 495
 Tyr Lys Val Val Leu Ala Pro Glu Thr Gly Glu Leu Lys Ser Val Ala
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 Arg Ile Val Leu Val Pro Asn Lys Lys Val Gly Leu Gln Phe Leu Gln
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 Arg Gln Cys
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<210> 87
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 <212> DNA
 <213> Mus musculus

<220>
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 polypeptide 1 (Cyp27a1), sterol 27-dehydrogenase
 (CYP27) cDNA

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<210> 88
 <211> 437
 <212> PRT
 <213> Mus musculus

<220>
 <223> mouse cytochrome P450, family 27, subfamily a,
 polypeptide 1 (Cyp27a1), sterol 27-dehydrogenase
 (CYP27)

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 35 40 45
 Thr Tyr Gly Ile Phe Ile Ala Gln Gly Glu Gln Trp Tyr His Leu Arg
 50 55 60
 Gln Ala Leu Lys Gln Arg Leu Leu Lys Pro Asp Glu Ala Ala Leu Tyr
 65 70 75 80
 Thr Asp Ala Leu Asn Glu Val Ile Ser Asp Phe Ile Thr Arg Leu Asp
 85 90 95
 Gln Val Arg Ala Glu Ser Glu Ser Gly Asp Gln Val Pro Asp Met Ala
 100 105 110
 His Leu Leu Tyr His Leu Ala Leu Glu Ala Ile Thr Tyr Ile Leu Phe
 115 120 125
 Glu Lys Arg Ile Gly Cys Leu Lys Pro Ser Ile Pro Glu Asp Thr Ala
 130 135 140
 Ala Phe Ile Arg Ser Val Ala Ile Met Phe Gln Asn Ser Val Tyr Ile
 145 150 155 160
 Thr Phe Leu Pro Lys Trp Thr Arg Pro Leu Leu Pro Phe Trp Lys Arg
 165 170 175

Tyr Leu Asn Gly Trp Asp Asn Ile Phe Ser Phe Gly Lys Lys Leu Ile
 180 185 190
 Asp Glu Lys Val Gln Glu Leu Lys Ala Gln Leu Gln Glu Thr Gly Pro
 195 200 205
 Asp Gly Val Arg Val Ser Gly Tyr Leu His Phe Leu Leu Thr Asn Glu
 210 215 220
 Leu Leu Ser Thr Gln Glu Thr Ile Gly Thr Phe Pro Glu Leu Leu Leu
 225 230 235 240
 Ala Gly Val Asp Thr Thr Ser Asn Thr Leu Thr Trp Ala Leu Tyr His
 245 250 255
 Leu Ser Lys Ser Pro Glu Ile Gln Glu Ala Leu His Lys Glu Val Thr
 260 265 270
 Gly Val Val Pro Phe Gly Lys Val Pro Gln His Lys Asp Phe Ala His
 275 280 285
 Met Pro Leu Leu Lys Ala Val Ile Lys Glu Thr Leu Arg Leu Tyr Pro
 290 295 300
 Val Val Pro Thr Asn Ser Arg Ile Ile Thr Glu Lys Glu Thr Glu Ile
 305 310 315 320
 Asn Gly Phe Leu Phe Pro Lys Asn Thr Gln Phe Val Leu Cys His Tyr
 325 330 335
 Val Val Ser Arg Asp Pro Ser Val Phe Pro Glu Pro Asn Ser Phe Gln
 340 345 350
 Pro His Arg Trp Leu Arg Lys Lys Glu Ala Asp Asn Pro Gly Ile Leu
 355 360 365
 His Pro Phe Gly Ser Val Pro Phe Gly Tyr Gly Val Arg Ser Cys Leu
 370 375 380
 Gly Arg Arg Ile Ala Glu Leu Glu Met Gln Leu Met Leu Ser Arg Leu
 385 390 395 400
 Val Gln Lys Tyr Glu Ile Ala Leu Ala Pro Gly Met Gly Glu Val Lys
 405 410 415
 Thr Val Ser Arg Ile Val Leu Val Pro Ser Lys Lys Val Arg Leu His
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 Phe Leu Gln Arg Gln
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<211> 1900

<212> DNA

<213> Rattus norvegicus

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 <223> CYP27

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<210> 90
 <211> 533
 <212> PRT
 <213> Rattus norvegicus

<220>
 <223> rat sterol 27-dehydrogenase (CYP27)

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 20 25 30
 Ala Ile Pro Ala Ala Leu Arg Asp His Glu Ser Thr Glu Gly Pro Gly
 35 40 45
 Thr Gly Gln Asp Arg Pro Arg Leu Arg Ser Leu Ala Glu Leu Pro Gly
 50 55 60

Pro	Gly	Thr	Leu	Arg	Phe	Leu	Phe	Gln	Leu	Phe	Leu	Arg	Gly	Tyr	Val	
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Leu	His	Leu	His	Glu	Leu	Gln	Ala	Leu	Asn	Lys	Ala	Lys	Tyr	Gly	Pro	
				85					90					95		
Met	Trp	Thr	Thr	Thr	Phe	Gly	Thr	Arg	Thr	Asn	Val	Asn	Leu	Ala	Ser	
			100					105					110			
Ala	Pro	Leu	Leu	Glu	Gln	Val	Met	Arg	Gln	Glu	Gly	Lys	Tyr	Pro	Ile	
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Arg	Asp	Ser	Met	Glu	Gln	Trp	Lys	Glu	His	Arg	Asp	His	Lys	Gly	Leu	
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Ser	Tyr	Gly	Ile	Phe	Ile	Thr	Gln	Gly	Gln	Gln	Trp	Tyr	His	Leu	Arg	
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His	Ser	Leu	Asn	Gln	Arg	Met	Leu	Lys	Pro	Ala	Glu	Ala	Ala	Leu	Tyr	
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Thr	Asp	Ala	Leu	Asn	Glu	Val	Ile	Ser	Asp	Phe	Ile	Ala	Arg	Leu	Asp	
			180					185					190			
Gln	Val	Arg	Thr	Glu	Ser	Ala	Ser	Gly	Asp	Gln	Val	Pro	Asp	Val	Ala	
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His	Leu	Leu	Tyr	His	Leu	Ala	Leu	Glu	Ala	Ile	Cys	Tyr	Ile	Leu	Phe	
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Thr	Phe	Leu	Pro	Lys	Trp	Ser	Arg	Pro	Leu	Leu	Pro	Phe	Trp	Lys	Arg	
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Tyr	Met	Asn	Asn	Trp	Asp	Asn	Ile	Phe	Ser	Phe	Gly	Glu	Lys	Met	Ile	
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His	Gln	Lys	Val	Gln	Glu	Ile	Glu	Ala	Gln	Leu	Gln	Ala	Ala	Gly	Pro	
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Leu	Leu	Ser	Pro	Gln	Glu	Thr	Val	Gly	Thr	Phe	Pro	Glu	Leu	Ile	Leu	
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Ala	Gly	Val	Asp	Thr	Thr	Ser	Asn	Thr	Leu	Thr	Trp	Ala	Leu	Tyr	His	
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Gly	Val	Val	Pro	Phe	Gly	Lys	Val	Pro	Gln	Asn	Lys	Asp	Phe	Ala	His	
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 Val Val Pro Thr Asn Ser Arg Ile Ile Thr Glu Lys Glu Thr Glu Ile
 405 410 415
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 Val Val Ser Arg Asp Pro Ser Val Phe Pro Glu Pro Glu Ser Phe Gln
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 Pro His Arg Trp Leu Arg Lys Arg Glu Asp Asp Asn Ser Gly Ile Gln
 450 455 460
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 Gly Arg Arg Ile Ala Glu Leu Glu Met Gln Leu Leu Leu Ser Arg Leu
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 <213> Homo sapiens

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 <223> endothelin A receptor

<220>
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 <222> (1341)..(1342)
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 <220>
 <223> human endothelin A receptor

 <220>
 <221> MOD_RES
 <222> (286)
 <223> Xaa = any amino acid

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 35 40 45
 Val Thr Thr His Gln Pro Thr Asn Leu Val Leu Pro Ser Asn Gly Ser
 50 55 60
 Met His Asn Tyr Cys Pro Gln Gln Thr Lys Ile Thr Ser Ala Phe Lys
 65 70 75 80
 Tyr Ile Asn Thr Val Ile Ser Cys Thr Ile Phe Ile Val Gly Met Val
 85 90 95
 Gly Asn Ala Thr Leu Leu Arg Ile Ile Tyr Gln Asn Lys Cys Met Arg
 100 105 110
 Asn Gly Pro Asn Ala Leu Ile Ala Ser Leu Ala Leu Gly Asp Leu Ile
 115 120 125
 Tyr Val Val Ile Asp Leu Pro Ile Asn Val Phe Lys Leu Leu Ala Gly
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 Arg Trp Pro Phe Asp His Asn Asp Phe Gly Val Phe Leu Cys Lys Leu
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 Phe Pro Phe Leu Gln Lys Ser Ser Val Gly Ile Thr Val Leu Asn Leu
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 Cys Ala Leu Ser Val Asp Arg Tyr Arg Ala Val Ala Ser Trp Ser Arg
 180 185 190
 Val Gln Gly Ile Gly Ile Pro Leu Val Thr Ala Ile Glu Ile Val Ser
 195 200 205
 Ile Trp Ile Leu Ser Phe Ile Leu Ala Ile Pro Glu Ala Ile Gly Phe
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 Val Met Val Pro Phe Glu Tyr Arg Gly Glu Gln His Lys Thr Cys Met
 225 230 235 240
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 245 250 255

Trp Trp Leu Phe Gly Phe Tyr Phe Cys Met Pro Leu Val Cys Thr Ala
 260 265 270
 Ile Phe Tyr Thr Leu Met Thr Cys Glu Met Leu Asn Arg Xaa Asn Gly
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 Ala Lys Thr Val Phe Cys Leu Val Val Ile Phe Ala Leu Cys Trp Phe
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 <223> endothelin A receptor

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<210> 94

<211> 427

<212> PRT

<213> Mus musculus

<220>

<223> mouse endothelin receptor type A

<400> 94

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Met Ser Ile Phe Cys Leu Ala Ala Tyr Phe Trp Leu Thr Met Val Gly
  1                      5                      10                      15

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Gly Val Met Ala Asp Asn Pro Glu Arg Tyr Ser Ala Asn Leu Ser Ser
          20                      25                      30

```

```

His Met Glu Asp Phe Thr Pro Phe Pro Gly Thr Glu Ile Asn Phe Leu
      35                      40                      45

```

```

Gly Thr Thr His Arg Pro Pro Asn Leu Ala Leu Pro Ser Asn Gly Ser
      50                      55                      60

```

```

Met His Gly Tyr Cys Pro Gln Gln Thr Lys Ile Thr Thr Ala Phe Lys
      65                      70                      75                      80

```

```

Tyr Ile Asn Thr Val Ile Ser Cys Thr Ile Phe Ile Val Gly Met Val
          85                      90                      95

```

Gly	Asn	Ala	Thr	Leu	Leu	Arg	Ile	Ile	Tyr	Gln	Asn	Lys	Cys	Met	Arg	100	105	110
Asn	Gly	Pro	Asn	Ala	Leu	Ile	Ala	Ser	Leu	Ala	Leu	Gly	Asp	Leu	Ile	115	120	125
Tyr	Val	Val	Ile	Asp	Leu	Pro	Ile	Asn	Val	Phe	Lys	Leu	Leu	Ala	Gly	130	135	140
Arg	Trp	Pro	Phe	Asp	His	Asn	Asp	Phe	Gly	Val	Phe	Leu	Cys	Lys	Leu	145	150	155
Phe	Pro	Phe	Leu	Gln	Lys	Ser	Ser	Val	Gly	Ile	Thr	Val	Leu	Asn	Leu	165	170	175
Cys	Ala	Leu	Ser	Val	Asp	Arg	Tyr	Arg	Ala	Val	Ala	Ser	Trp	Ser	Arg	180	185	190
Val	Gln	Gly	Ile	Gly	Ile	Pro	Leu	Ile	Thr	Ala	Ile	Glu	Ile	Val	Ser	195	200	205
Ile	Trp	Ile	Leu	Ser	Phe	Ile	Leu	Ala	Ile	Pro	Glu	Ala	Ile	Gly	Phe	210	215	220
Val	Met	Val	Pro	Phe	Glu	Tyr	Lys	Gly	Glu	Leu	His	Arg	Thr	Cys	Met	225	230	235
Leu	Asn	Ala	Thr	Ser	Lys	Phe	Met	Glu	Phe	Tyr	Gln	Asp	Val	Lys	Asp	245	250	255
Trp	Trp	Leu	Phe	Gly	Phe	Tyr	Phe	Cys	Met	Pro	Leu	Val	Cys	Thr	Ala	260	265	270
Ile	Phe	Tyr	Thr	Leu	Met	Thr	Cys	Glu	Met	Leu	Asn	Arg	Arg	Asn	Gly	275	280	285
Ser	Leu	Arg	Ile	Ala	Leu	Ser	Glu	His	Leu	Lys	Gln	Arg	Arg	Glu	Val	290	295	300
Ala	Lys	Thr	Val	Phe	Cys	Leu	Val	Val	Ile	Phe	Ala	Leu	Cys	Trp	Phe	305	310	315
Pro	Leu	His	Leu	Ser	Arg	Ile	Leu	Lys	Lys	Thr	Val	Tyr	Asp	Glu	Met	325	330	335
Asp	Lys	Asn	Arg	Cys	Glu	Leu	Leu	Ser	Phe	Leu	Leu	Leu	Met	Asp	Tyr	340	345	350
Ile	Gly	Ile	Asn	Leu	Ala	Thr	Met	Asn	Ser	Cys	Ile	Asn	Pro	Ile	Ala	355	360	365
Leu	Tyr	Phe	Val	Ser	Lys	Lys	Phe	Lys	Asn	Cys	Phe	Gln	Ser	Cys	Leu	370	375	380
Cys	Cys	Cys	Cys	His	Gln	Ser	Lys	Ser	Leu	Met	Thr	Ser	Val	Pro	Met	385	390	395

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405 410 415

Thr Glu Arg Ser Ser His Lys Asp Ser Met Asn
420 425

<210> 95
<211> 1436
<212> DNA
<213> Rattus norvegicus

<220>
<223> rat endothelin receptor type A cDNA

<220>
<221> CDS
<222> (44)..(1324)
<223> endothelin A receptor

<400> 95
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cagtgttaat ctaagcagcc acgtggagga cttcacccct tttccaggga cagagttcga 180
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<210> 96
<211> 426
<212> PRT
<213> Rattus norvegicus

<220>
<223> rat endothelin receptor type A

<400> 96
Met Gly Val Leu Cys Phe Leu Ala Ser Phe Trp Leu Ala Leu Val Gly
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Gly Ala Ile Ala Asp Asn Ala Glu Arg Tyr Ser Ala Asn Leu Ser Ser
20 25 30

His Val Glu Asp Phe Thr Pro Phe Pro Gly Thr Glu Phe Asp Phe Leu
 35 40 45
 Gly Thr Thr Leu Arg Pro Pro Asn Leu Ala Leu Pro Ser Asn Gly Ser
 50 55 60
 Met His Gly Tyr Cys Pro Gln Gln Thr Lys Ile Thr Thr Ala Phe Lys
 65 70 75 80
 Tyr Ile Asn Thr Val Ile Ser Cys Thr Ile Phe Ile Val Gly Met Val
 85 90 95
 Gly Asn Ala Thr Leu Leu Arg Ile Ile Tyr Gln Asn Lys Cys Met Arg
 100 105 110
 Asn Gly Pro Asn Ala Leu Ile Ala Ser Leu Ala Leu Gly Asp Leu Ile
 115 120 125
 Tyr Val Val Ile Asp Leu Pro Ile Asn Val Phe Lys Leu Leu Ala Gly
 130 135 140
 Arg Trp Pro Phe Asp His Asn Asp Phe Gly Val Phe Leu Cys Lys Leu
 145 150 155 160
 Phe Pro Phe Leu Gln Lys Ser Ser Val Gly Ile Thr Val Leu Asn Leu
 165 170 175
 Cys Ala Leu Ser Val Asp Arg Tyr Arg Ala Val Ala Ser Trp Ser Arg
 180 185 190
 Val Gln Gly Ile Gly Ile Pro Leu Ile Thr Ala Ile Glu Ile Val Ser
 195 200 205
 Ile Trp Ile Leu Ser Phe Ile Leu Ala Ile Pro Glu Ala Ile Gly Phe
 210 215 220
 Val Met Val Pro Phe Glu Tyr Lys Gly Glu Gln His Arg Thr Cys Met
 225 230 235 240
 Leu Asn Ala Thr Thr Lys Phe Met Glu Phe Tyr Gln Asp Val Lys Asp
 245 250 255
 Trp Trp Leu Phe Gly Phe Tyr Phe Cys Met Pro Leu Val Cys Thr Ala
 260 265 270
 Ile Phe Tyr Thr Leu Met Thr Cys Glu Met Leu Asn Arg Arg Asn Gly
 275 280 285
 Ser Leu Arg Ile Ala Leu Ser Glu His Leu Lys Gln Arg Arg Glu Val
 290 295 300
 Ala Lys Thr Val Phe Cys Leu Val Val Ile Phe Ala Leu Cys Trp Phe
 305 310 315 320
 Pro Leu His Leu Ser Arg Ile Leu Lys Lys Thr Val Tyr Asp Glu Met
 325 330 335
 Asp Lys Asn Arg Cys Glu Leu Leu Ser Phe Leu Leu Leu Met Asp Tyr
 340 345 350

Ile Gly Ile Asn Leu Ala Thr Met Asn Ser Cys Ile Asn Pro Ile Ala
 355 360 365
 Leu Tyr Phe Val Ser Lys Lys Phe Lys Asn Cys Phe Gln Ser Cys Leu
 370 375 380
 Cys Cys Cys Cys His Gln Ser Lys Ser Leu Met Thr Ser Val Pro Met
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 Glu Arg Ser Ser His Lys Asp Ser Met Asn
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<210> 97
 <211> 2360
 <212> DNA
 <213> Homo sapiens

<220>
 <223> human heparin-binding epidermal growth factor
 (EGF)-like growth factor cDNA

<220>
 <221> CDS
 <222> (262)..(888)
 <223> EGF-like

<400> 97
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 gttaactgtg aaataaccaca agcctgagaa ctgaattttg ggacttctac ccagatggaa 1440
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 gtctgtctac atttctgcag atcttccgtg gtcagagtgc cactgcggga gctctgtatg 1740
 gtcaggatgt aggggttaac ttggctcagag ccactctatg agttggactt cagtcttgcc 1800

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<210> 98

<211> 208

<212> PRT

<213> Homo sapiens

<220>

<223> human heparin-binding epidermal growth factor
(EGF)-like growth factor

<400> 98

```

Met Lys Leu Leu Pro Ser Val Val Leu Lys Leu Phe Leu Ala Ala Val
  1                      5                      10                      15

```

```

Leu Ser Ala Leu Val Thr Gly Glu Ser Leu Glu Arg Leu Arg Arg Gly
          20                      25                      30

```

```

Leu Ala Ala Gly Thr Ser Asn Pro Asp Pro Pro Thr Val Ser Thr Asp
          35                      40                      45

```

```

Gln Leu Leu Pro Leu Gly Gly Gly Arg Asp Arg Lys Val Arg Asp Leu
          50                      55                      60

```

```

Gln Glu Ala Asp Leu Asp Leu Leu Arg Val Thr Leu Ser Ser Lys Pro
          65                      70                      75                      80

```

```

Gln Ala Leu Ala Thr Pro Asn Lys Glu Glu His Gly Lys Arg Lys Lys
          85                      90                      95

```

```

Lys Gly Lys Gly Leu Gly Lys Lys Arg Asp Pro Cys Leu Arg Lys Tyr
          100                      105                      110

```

```

Lys Asp Phe Cys Ile His Gly Glu Cys Lys Tyr Val Lys Glu Leu Arg
          115                      120                      125

```

```

Ala Pro Ser Cys Ile Cys His Pro Gly Tyr His Gly Glu Arg Cys His
          130                      135                      140

```

```

Gly Leu Ser Leu Pro Val Glu Asn Arg Leu Tyr Thr Tyr Asp His Thr
          145                      150                      155                      160

```

```

Thr Ile Leu Ala Val Val Ala Val Val Leu Ser Ser Val Cys Leu Leu
          165                      170                      175

```

```

Val Ile Val Gly Leu Leu Met Phe Arg Tyr His Arg Arg Gly Gly Tyr
          180                      185                      190

```

```

Asp Val Glu Asn Glu Glu Lys Val Lys Leu Gly Met Thr Asn Ser His
          195                      200                      205

```

<210> 99
 <211> 2337
 <212> DNA
 <213> Mus musculus

<220>
 <223> mouse heparin-binding epidermal growth factor
 (EGF)-like growth factor cDNA

<220>
 <221> CDS
 <222> (262)..(888)
 <223> EGF-like

<400> 99
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<210> 100
 <211> 208
 <212> PRT
 <213> Mus musculus

<220>
 <223> mouse heparin-binding epidermal growth factor
 (EGF)-like growth factor

<400> 100
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 Leu Ser Ala Leu Val Thr Gly Glu Ser Leu Glu Arg Leu Arg Arg Gly
 20 25 30
 Leu Ala Ala Ala Thr Ser Asn Pro Asp Pro Pro Thr Gly Ser Thr Asn
 35 40 45
 Gln Leu Leu Pro Thr Gly Gly Asp Arg Ala Gln Gly Val Gln Asp Leu
 50 55 60
 Glu Gly Thr Asp Leu Asn Leu Phe Lys Val Ala Phe Ser Ser Lys Pro
 65 70 75 80
 Gln Gly Leu Ala Thr Pro Ser Lys Glu Arg Asn Gly Lys Lys Lys Lys
 85 90 95
 Lys Gly Lys Gly Leu Gly Lys Lys Arg Asp Pro Cys Leu Arg Lys Tyr
 100 105 110
 Lys Asp Tyr Cys Ile His Gly Glu Cys Arg Tyr Leu Gln Glu Phe Arg
 115 120 125
 Thr Pro Ser Cys Lys Cys Leu Pro Gly Tyr His Gly His Arg Cys His
 130 135 140
 Gly Leu Thr Leu Pro Val Glu Asn Pro Leu Tyr Thr Tyr Asp His Thr
 145 150 155 160
 Thr Val Leu Ala Val Val Ala Val Val Leu Ser Ser Val Cys Leu Leu
 165 170 175
 Val Ile Val Gly Leu Leu Met Phe Arg Tyr His Arg Arg Gly Gly Tyr
 180 185 190
 Asp Leu Glu Ser Glu Glu Lys Val Lys Leu Gly Val Ala Ser Ser His
 195 200 205

<210> 101
 <211> 1550
 <212> DNA
 <213> Rattus norvegicus

<220>
 <223> rat heparin-binding epidermal growth factor
 (EGF)-like growth factor cDNA

<220>
 <221> CDS
 <222> (32)..(658)
 <223> EGF-like

<400> 101
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<210> 102

<211> 208

<212> PRT

<213> *Rattus norvegicus*

<220>

<223> rat heparin-binding epidermal growth factor
(EGF)-like growth factor

<400> 102

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Gln Leu Leu Pro Thr Gly Ala Asp Arg Ala Gln Glu Val Gln Asp Leu
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Glu Gly Thr Asp Leu Asp Leu Phe Lys Val Ala Phe Ser Ser Lys Pro
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Gln Ala Leu Ala Thr Pro Gly Lys Glu Lys Asn Gly Lys Lys Lys Arg
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Lys Asp Tyr Cys Ile His Gly Glu Cys Arg Tyr Leu Lys Glu Leu Arg
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 Gly Leu Thr Leu Pro Val Glu Asn Pro Leu Tyr Thr Tyr Asp His Thr
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 Thr Val Leu Ala Val Val Ala Val Val Leu Ser Ser Val Cys Leu Leu
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<212> PRT

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<223> human MET proto-oncogene (TRP-MET)

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Val	Ala	Glu	Tyr	Lys	Thr	Gly	Pro	Val	Leu	Glu	His	Pro	Asp	Cys	Phe	85	90	95	
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 Tyr Val Asn Asp Phe Phe Asn Lys Ile Val Asn Lys Asn Asn Val Arg
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 385 390 395 400
 Thr Leu Leu Arg Asn Ser Ser Gly Cys Glu Ala Arg Arg Asp Glu Tyr
 405 410 415
 Arg Thr Glu Phe Thr Thr Ala Leu Gln Arg Val Asp Leu Phe Met Gly
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 Asp Leu Thr Ile Ala Asn Leu Gly Thr Ser Glu Gly Arg Phe Met Gln
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 Val Val Val Ser Arg Ser Gly Pro Ser Thr Pro His Val Asn Phe Leu
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 Leu Asp Ser His Pro Val Ser Pro Glu Val Ile Val Glu His Thr Leu
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<211> 1379

<212> PRT

<213> Mus musculus

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<223> mouse MET proto-oncogene (TRP-MET)

<400> 106

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Cys	Thr	Leu	Thr	Leu	Ser	Glu	Ser	Thr	Thr	Asn	Thr	Leu	Lys	Cys	Thr	610	615	620
Val	Gly	Pro	Ala	Met	Ser	Glu	His	Phe	Asn	Val	Ser	Val	Ile	Ile	Ser	625	630	635
Asn	Ser	Arg	Glu	Thr	Thr	Gln	Tyr	Ser	Ala	Phe	Ser	Tyr	Val	Asp	Pro	645	650	655
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 Val Lys Leu Lys Ile Asp Leu Ala Asn Arg Glu Thr Ser Ser Phe Ser
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<211> 1382

<212> PRT

<213> Rattus norvegicus

<220>

<223> rat MET proto-oncogene (TRP-MET)

<400> 108

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Glu Thr Pro Ile Gln Asn Val Val Leu His Gly His His Ile Tyr Leu
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Lys	Tyr	Val	Asn	Asp	Phe	Phe	Asn	Lys	Ile	Val	Asn	Lys	Asn	Asn	Val	370	375	380	

Arg	Cys	Leu	Gln	His	Phe	Tyr	Gly	Pro	Asn	His	Glu	His	Cys	Phe	Asn	385	390	395	400
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Tyr	Arg	Thr	Glu	Phe	Thr	Thr	Ala	Leu	Gln	Ala	Val	Asp	Leu	Phe	Met	420	425	430	
Gly	Arg	Leu	Asn	His	Val	Leu	Leu	Thr	Ser	Ile	Ser	Thr	Phe	Ile	Lys	435	440	445	
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Leu	Leu	Asp	Ser	His	Pro	Val	Ser	Pro	Glu	Val	Ile	Val	Glu	His	Pro	485	490	495	
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Ile	Cys	Leu	Pro	Ala	Val	Tyr	Lys	Val	Phe	Pro	Thr	Ser	Ala	Pro	Leu	565	570	575	
Glu	Gly	Gly	Thr	Met	Leu	Thr	Ile	Cys	Gly	Trp	Asp	Phe	Gly	Phe	Lys	580	585	590	
Lys	Asn	Asn	Lys	Phe	Asp	Leu	Arg	Lys	Thr	Lys	Val	Leu	Leu	Gly	Asn	595	600	605	
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Gly	Thr	Leu	Leu	Thr	Leu	Thr	Gly	Lys	Tyr	Leu	Asn	Ser	Gly	Asn	Ser	675	680	685	
Arg	His	Ile	Ser	Ile	Gly	Gly	Lys	Thr	Cys	Thr	Leu	Lys	Ser	Val	Ser	690	695	700	

Asp	Ser	Ile	Leu	Glu	Cys	Tyr	Thr	Pro	Gly	His	Thr	Val	Ser	Ala	Glu	705	710	715	720
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Trp Arg Leu Thr Arg Glu Arg Arg Glu Ala Pro Arg Pro Tyr Ser Lys
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Gln Val Ser Tyr Val Ile Gln Ala Glu Gly Lys Glu His Ile Ile His
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```

<210> 112

<211> 845

<212> PRT

<213> Mus musculus

<220>

<223> mouse a disintegrin and metalloproteinase domain 9
(MDC9) (meltrin gamma, Adam9)

<400> 112

Met Gly Pro Arg Ala Leu Ser Pro Leu Ala Ser Leu Arg Leu Arg Trp
1 5 10 15

Leu Leu Ala Cys Gly Leu Leu Gly Pro Val Leu Glu Ala Gly Arg Pro
20 25 30

Asp Leu Glu Gln Thr Val His Leu Ser Ser Tyr Glu Ile Ile Thr Pro
35 40 45

Trp Arg Leu Thr Arg Glu Arg Arg Glu Ala Leu Gly Pro Ser Ser Gln
50 55 60

Gln Ile Ser Tyr Val Ile Gln Ala Gln Gly Lys Gln His Ile Ile His
65 70 75 80

Leu Glu Arg Asn Thr Asp Leu Leu Pro Asn Asp Phe Val Val Tyr Thr
 85 90 95
 Tyr Asp Lys Glu Gly Ser Leu Leu Ser Asp His Pro Asn Val Gln Ser
 100 105 110
 His Cys His Tyr Arg Gly Tyr Val Glu Gly Val Gln Asn Ser Ala Val
 115 120 125
 Ala Val Ser Ala Cys Phe Gly Leu Arg Gly Leu Leu His Leu Glu Asn
 130 135 140
 Ala Ser Phe Gly Ile Glu Pro Leu His Asn Ser Ser His Phe Glu His
 145 150 155 160
 Ile Phe Tyr Pro Met Asp Gly Ile His Gln Glu Pro Leu Arg Cys Gly
 165 170 175
 Val Ser Asn Arg Asp Thr Glu Lys Glu Gly Thr Gln Gly Asp Glu Glu
 180 185 190
 Glu His Pro Ser Val Thr Gln Leu Leu Arg Arg Arg Arg Ala Val Leu
 195 200 205
 Pro Gln Thr Arg Tyr Val Glu Leu Phe Ile Val Val Asp Lys Glu Arg
 210 215 220
 Tyr Asp Met Met Gly Arg Asn Gln Thr Ala Val Arg Glu Glu Met Ile
 225 230 235 240
 Arg Leu Ala Asn Tyr Leu Asp Ser Met Tyr Ile Met Leu Asn Ile Arg
 245 250 255
 Ile Val Leu Val Gly Leu Glu Ile Trp Thr Asp Arg Asn Pro Ile Asn
 260 265 270
 Ile Ile Gly Gly Ala Gly Asp Val Leu Gly Asn Phe Val Gln Trp Arg
 275 280 285
 Glu Lys Phe Leu Ile Thr Arg Arg Arg His Asp Ser Ala Gln Leu Val
 290 295 300
 Leu Lys Lys Gly Phe Gly Gly Thr Ala Gly Met Ala Phe Val Gly Thr
 305 310 315 320
 Val Cys Ser Arg Ser His Ala Gly Gly Ile Asn Val Phe Gly Gln Ile
 325 330 335
 Thr Val Glu Thr Phe Ala Ser Ile Val Ala His Glu Leu Gly His Asn
 340 345 350
 Leu Gly Met Asn His Asp Asp Gly Arg Glu Cys Phe Cys Gly Ala Lys
 355 360 365
 Ser Cys Ile Met Asn Ser Gly Ala Ser Gly Ser Arg Asn Phe Ser Ser
 370 375 380
 Cys Ser Ala Glu Asp Phe Glu Lys Leu Thr Leu Asn Lys Gly Gly Ser
 385 390 395 400

Cys	Leu	Leu	Asn	Ile	Pro	Lys	Pro	Asp	Glu	Ala	Tyr	Ser	Ala	Pro	Ser		
				405						410				415			
Cys	Gly	Asn	Lys	Leu	Val	Asp	Pro	Gly	Glu	Glu	Cys	Asp	Cys	Gly	Thr		
			420					425						430			
Ala	Lys	Glu	Cys	Glu	Val	Asp	Pro	Cys	Cys	Glu	Gly	Ser	Thr	Cys	Lys		
		435					440						445				
Leu	Lys	Ser	Phe	Ala	Glu	Cys	Ala	Tyr	Gly	Asp	Cys	Cys	Lys	Asp	Cys		
	450					455					460						
Gln	Phe	Leu	Pro	Gly	Gly	Ser	Met	Cys	Arg	Gly	Lys	Thr	Ser	Glu	Cys		
465					470					475					480		
Asp	Val	Pro	Glu	Tyr	Cys	Asn	Gly	Ser	Ser	Gln	Phe	Cys	Pro	Pro	Asp		
				485					490					495			
Val	Phe	Ile	Gln	Asn	Gly	Tyr	Pro	Cys	Gln	Asn	Ser	Lys	Ala	Tyr	Cys		
			500					505					510				
Tyr	Asn	Gly	Met	Cys	Gln	Tyr	Tyr	Asp	Ala	Gln	Cys	Gln	Val	Ile	Phe		
	515						520						525				
Gly	Ser	Lys	Ala	Lys	Ala	Ala	Pro	Arg	Asp	Cys	Phe	Ile	Glu	Val	Asn		
	530					535					540						
Ser	Lys	Gly	Asp	Arg	Phe	Gly	Asn	Cys	Gly	Phe	Ser	Gly	Ser	Glu	Tyr		
545					550					555					560		
Lys	Lys	Cys	Ala	Thr	Gly	Asn	Ala	Leu	Cys	Gly	Lys	Leu	Gln	Cys	Glu		
				565					570					575			
Asn	Val	Gln	Asp	Met	Pro	Val	Phe	Gly	Ile	Val	Pro	Ala	Ile	Ile	Gln		
			580					585					590				
Thr	Pro	Ser	Arg	Gly	Thr	Lys	Cys	Trp	Gly	Val	Asp	Phe	Gln	Leu	Gly		
		595					600					605					
Ser	Asp	Val	Pro	Asp	Pro	Gly	Met	Val	Asn	Glu	Gly	Thr	Lys	Cys	Asp		
	610					615					620						
Ala	Gly	Lys	Ile	Cys	Arg	Asn	Phe	Gln	Cys	Val	Asn	Ala	Ser	Val	Leu		
625					630					635					640		
Asn	Tyr	Asp	Cys	Asp	Ile	Gln	Gly	Lys	Cys	His	Gly	His	Gly	Val	Cys		
				645					650					655			
Asn	Ser	Asn	Lys	Asn	Cys	His	Cys	Glu	Asp	Gly	Trp	Ala	Pro	Pro	His		
			660					665					670				
Cys	Asp	Thr	Lys	Gly	Tyr	Gly	Gly	Ser	Val	Asp	Ser	Gly	Pro	Thr	Tyr		
		675					680					685					
Asn	Ala	Lys	Ser	Thr	Ala	Leu	Arg	Asp	Gly	Leu	Leu	Val	Phe	Phe	Phe		
	690					695					700						
Leu	Ile	Val	Pro	Leu	Val	Ala	Ala	Ala	Ile	Phe	Leu	Phe	Ile	Lys	Arg		
705					710					715					720		

Asp Glu Leu Arg Lys Thr Phe Arg Lys Lys Arg Ser Gln Met Ser Asp
 725 730 735
 Gly Arg Asn Gln Ala Asn Val Ser Arg Gln Pro Gly Asp Pro Ser Ile
 740 745 750
 Ser Arg Pro Pro Gly Gly Pro Asn Val Ser Arg Pro Pro Gly Gly Pro
 755 760 765
 Gly Val Ser Arg Pro Pro Gly Gly Pro Gly Val Ser Arg Pro Pro Gly
 770 775 780
 Gly Pro Gly Val Ser Arg Pro Pro Pro Gly His Gly Asn Arg Phe Pro
 785 790 795 800
 Val Pro Thr Tyr Ala Ala Lys Gln Pro Ala Gln Phe Pro Ser Arg Pro
 805 810 815
 Pro Pro Pro Gln Pro Lys Ile Ser Ser Gln Gly Asn Leu Ile Pro Ala
 820 825 830
 Arg Pro Ala Pro Ala Pro Pro Leu Tyr Ser Ser Leu Thr
 835 840 845

<210> 113
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:hexahistidine
 (His) affinity tag

<400> 113
 His His His His His His
 1 5

<210> 114
 <211> 200
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:poly-Gly
 flexible linker

<220>
 <221> MOD_RES
 <222> (6)..(200)
 <223> Gly residues from position 6 to 200 may be present
 or absent

<400> 114
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 20 25 30

Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 35 40 45
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 50 55 60
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 65 70 75 80
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 85 90 95
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 100 105 110
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 115 120 125
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 130 135 140
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 145 150 155 160
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 165 170 175
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 180 185 190
 Gly Gly Gly Gly Gly Gly Gly Gly Gly
 195 200